GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:00:26 ; Search time 194 Seconds
(without alignments)
1256.986 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3107	100.0	555	3	AAY52523	Aay52523 House dus
2	3107	100.0	555	5	AAU96327	Aau96327 Der HMW-m
3	3107	100.0	555	5	AAU96328	Aau96328 Der HMW-m
4	3014	97.0	536	3	AAY52525	Aay52525 House dus
5	3014	97.0	536	5	AAU96329	Aau96329 Der HMW-m
6	2542	81.8	509	3	AAY52533	Aay52533 D. pteron
7	2542	81.8	509	5	AAU96337	Aau96337 Der HMW-m
8	2542	81.8	509	5	AAU96338	Aau96338 Der HMW-m
9	2475	79.7	490	3	AAY52535	Aay52535 D. pteron
10	2475	79.7	490	5	AAU96339	Aau96339 Der HMW-m
11	1008.5	32.5	525	6	ABP72636	Abp72636 Anopheles
12	854.5	27.5	4498	4	ABB58595	Abb58595 Drosophil
13	838.5	27.0	554	2	AAW01824	Aaw01824 Manduca s
14	838.5	27.0	554	3	AAB07183	Aab07183 Manduca s
15	838.5	27.0	554	6	ABP72619	Abp72619 Manduca s
16	837.5	27.0	467	6	ABP72634	Abp72634 Prawn chi
17	837.5	27.0	565	6	ABP72625	Abp72625 Bombyx mo
18	837.5	27.0	595	4	ABB71737	Abb71737 Drosophil
19	832	26.8	460	4	ABB64366	Abb64366 Drosophil
20	815.5	26.2	583	5	AAE28197	Aae28197 Flea chit
21	812.5	26.2	635	5	AAE28203	Aae28203 Flea chit
22	811.5	26.1	559	5	AAE28199	Aae28199 Flea PCfC
23	810	26.1	574	6	ABP72635	Abp72635 Aedes aeg
24	802	25.8	483	6	ABP72633	Abp72633 Chelonus
25	787	25.3	553	6	ABP72626	Abp72626 Hyphantri
26	738	23.8	444	8	ADQ59635	Adq59635 Chitotrio
27	738	23.8	466	2	AAW08584	Aaw08584 Human 50
28	738	23.8	466	2	AAW40259	Aaw40259 Human chi
29	738	23.8	466	2	AAY42425	Aay42425 MO-218 cl
30	738	23.8	466	4	AAE00432	Aae00432 Human chi
31	738	23.8	466	5	AAE25903	Aae25903 Human chi
32	738	23.8	466	5	ABB76291	Abb76291 Human chi
33	738	23.8	466	7	ABW00767	Abw00767 Human chi
34	738	23.8	466	8	ADQ18533	Adq18533 Human sof
35	738	23.8	466	8	ADQ59634	Adq59634 Chitotrio
36	738	23.8	466	9	ADZ80444	Adz80444 Mature ch
37	737.5	23.7	520	6	ABU09914	Abu09914 Partial m
38	736.5	23.7	473	7	ABR55543	Abr55543 Amino aci
39	736.5	23.7	473	8	ADT92466	Adt92466 Murine ac
40	735.5	23.7	459	7	ADC24231	Adc24231 Human NOV
41	734.5	23.6	473	7	ADC51464	Adc51464 Chitotria
42	732.5	23.6	387	2	AAW08585	Aaw08585 Human 39
43	732	23.6	447	7	ADC24237	Adc24237 Human NOV
44	732	23.6	466	2	AAW40260	Aaw40260 Human chi
45	732	23.6	466	2	AAY42426	Aay42426 MO-13B cl

ALIGNMENTS

RESULT 1
AAY52523
ID AAY52523 standard; protein; 555 AA.
XX
AC AAY52523;
XX
DT 22-FEB-2000 (first entry)
XX
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.
XX
OS Dermatophagoides farinae.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /note= "Signal peptide"
FT Protein 20. .555
FT /note= "Mature PDerf98-555"
XX
PN WO9954349-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2000-052700/04.
DR N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
XX
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivy to mite allergens.
XX
PS Claim 3; Page 111-113; 154pp; English.
XX
CC This sequence represents Dermatophagoides farinae mite allergen protein
CC (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD,

CC comprising 555 amino acids, and is a component of the Dermatophagoides
CC farinae high molecular weight mite allergen protein (HWM-map)
CC composition. The HMW-map composition was isolated from a D. farinae
CC homogenate by gel filtration, with each fraction being analysed for the
CC presence of proteins that bound to IgE present in mite-allergic dog
CC antisera. Mite allergenic proteins and peptides, and nucleic acids
CC encoding them, may be used in therapeutic compositions to modify an
CC animal's hypersensitivity reaction to mite allergens. Animals that may be
CC treated include mammals and birds, especially felines, canines, equines,
CC humans, other pets, and work or domestic animals. The proteins or
CC fragments may also be used to diagnose allergies via a skin test. The
CC proteins and peptides can also be used to raise antibodies, which have a
CC variety of potential uses. For example, they can be used as vaccines to
CC passively immunise animals against dust mite hypersensitivity, as
CC positive controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e-217;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
```

RESULT 2
AAU96327
ID AAU96327 standard; protein; 555 AA.
XX
AC AAU96327;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #14.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69571.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 114-116; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e-217;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
```

RESULT 3
AAU96328
ID AAU96328 standard; protein; 555 AA.
XX
AC AAU96328;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #15.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69573.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 120-122; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 3107; DB 5; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e-217;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
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Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
```

RESULT 4
AAY52525
ID AAY52525 standard; protein; 536 AA.
XX
AC AAY52525;
XX
DT 22-FEB-2000 (first entry)
XX
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.
XX
OS Dermatophagoides farinae.
XX
PN WO9954349-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;

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XX
DR   WPI; 2000-052700/04.
DR   N-PSDB; AAZ38579, AAZ38580.
XX
PT   Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT   used to modify an animals' hypersensitivy to mite allergens.
XX
PS   Claim 3; Page 125-127; 154pp; English.
XX
CC   This sequence represents Dermatophagoides farinae mite allergen protein
CC   (map) PDerf98-536, the mature form of PDerf98-555 (AAY52523). PDerf98-536
CC   has a molecular weight of 98 kD, comprising 536 amino acids, and is a
CC   component of the Dermatophagoides farinae high molecular weight mite
CC   allergen protein (HWM-map) composition. The HMW-map composition was
CC   isolated from a D. farinae homogenate by gel filtration, with each
CC   fraction being analysed for the presence of proteins that bound to IgE
CC   present in mite-allergic dog antisera. Mite allergenic proteins and
CC   peptides, and nucleic acids encoding them, may be used in therapeutic
CC   compositions to modify an animal's hypersensitivity reaction to mite
CC   allergens. Animals that may be treated include mammals and birds,
CC   especially felines, canines, equines, humans, other pets, and work or
CC   domestic animals. The proteins or fragments may also be used to diagnose
CC   allergies via a skin test. The proteins and peptides can also be used to
CC   raise antibodies, which have a variety of potential uses. For example,
CC   they can be used as vaccines to passively immunise animals against dust
CC   mite hypersensitivity, as positive controls in test kits and as tools to
CC   recover desired dust mite allergens from a mixture of proteins
XX
SQ   Sequence 536 AA;

  Query Match             97.0%;  Score 3014;  DB 3;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-210;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 60

Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 420

Qy        440 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 480

Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536


RESULT 5
AAU96329
ID   AAU96329 standard; protein; 536 AA.
XX
AC   AAU96329;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Der HMW-map polypeptide #16.
XX
KW   Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW   mite allergenic protein; immunoglobulin E; hypersensitivity;
KW   immunocomplex formation.
XX
OS   Dermatophagoides farinae.
XX
PN   WO200222807-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028730.
XX
PR   14-SEP-2000; 2000US-00662293.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2002-351888/38.
DR   N-PSDB; ABK69575.
XX
PT   New mite allergenic protein isolated from Dermatophagoides, designated
PT   Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS   Claim 12; Page 125-127; 161pp; English.
XX
CC   The invention relates to an isolated mite allergenic protein of
CC   Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC   acid. The Der HMW-map protein is useful for eliciting an immune response
CC   against Der HMW-map protein. The protein or a reagent comprising a non-
CC   proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC   cat) susceptible to or having an allergic response to a mite. A
CC   therapeutic composition is useful for desensitising a host animal to an
CC   allergic response to a mite. The DNA and protein can be used in the
CC   detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC   of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC   disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC   binding of proteins to IgE, to prevent immunocomplex formation, thus
CC   reducing hypersensitivity responses to mite allergens, and as vaccines
CC   against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC   represent Der HMW-map polypeptides of the invention
XX
SQ   Sequence 536 AA;

  Query Match             97.0%;  Score 3014;  DB 5;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-210;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 60

Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTTPTTTPTTPSPT 439
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTTPTTTPTTPSPT 420

Qy        440 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 499
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 480

Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536
```

RESULT 6
AAY52533
ID AAY52533 standard; protein; 509 AA.
XX
AC AAY52533;
XX
DT 06-AUG-2003 (revised)
DT 22-FEB-2000 (first entry)
XX
DE D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IgE; immunoglobulin E; allergen; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.
XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /note= "Signal peptide"
FT Protein 20. .509
FT /note= "Mature PDerp98-509"
XX
PN WO9954349-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2000-052700/04.
DR N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.
XX
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivy to mite allergens.
XX
PS Claim 3; Page 134-136; 154pp; English.
XX
CC This sequence represents Dermatophagoides pteronyssius mite allergen
CC protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD,
CC comprising 509 amino acids, and has a high degree of homology with the D.
CC farinae 98 kD allergen, mapB (AAY52523). Nucleic acid molecules encoding
CC PDerp98-509 were isolated from a D. pteronyssius cDNA library by
CC hybridisation with a probe encoding the D. farinae high molecular weight
CC map (HMW-map) composition. Mite allergenic proteins and peptides, and
CC nucleic acids encoding them, may be used in therapeutic compositions to
CC modify an animal's hypersensitivity reaction to mite allergens. Animals
CC that may be treated include mammals and birds, especially felines,
CC canines, equines, humans, other pets, and work or domestic animals. The
CC proteins or fragments may also be used to diagnose allergies via a skin
CC test. The proteins and peptides can also be used to raise antibodies,
CC which have a variety of potential uses. For example, they can be used as
CC vaccines to passively immunise animals against dust mite
CC hypersensitivity, as positive controls in test kits and as tools to
CC recover desired dust mite allergens from a mixture of proteins. (Updated
CC on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 509 AA;

```
  Query Match             81.8%;  Score 2542;  DB 3;  Length 509;
  Best Local Similarity   81.7%;  Pred. No. 2.6e-176;
  Matches  456;  Conservative   24;  Mismatches   26;  Indels   52;  Gaps    2;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||| :|:  | ||||||||: |||||:||||||||||||||||||||||||||||||||||
Db          1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| ||
Db        121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||:|||| |||||||||||||||| ||::||||:|||||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              |||||||||||||:|||||||||||||| ||||||||||||||||:||:||||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||  || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                  |||||: |||||||||||:|||||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
              || || |      || |
Db        492 DCPKGTRWHATLKNCIQE 509
```

RESULT 7
AAU96337
ID AAU96337 standard; protein; 509 AA.
XX
AC AAU96337;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #24.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX

OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69581.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 134-136; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 509 AA;

Query Match 81.8%; Score 2542; DB 5; Length 509;
Best Local Similarity 81.7%; Pred. No. 2.6e-176;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

```
Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||| :|:  | ||||||||: |||||:||||||||||||||||||||||||||||||||
Db          1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              |||||||||||||||||||:|||||||||| ||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||| ||
Db        121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||:|||| |||||||||||||||| ||::||||:|||||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              |||||||||||||:|||||||||||||||| ||||||||||||||||:||:|||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||  || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
              ||||: |||||||||:|||||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
              || || |      || |
Db        492 DCPKGTRWHATLKNCIQE 509
```

RESULT 8
AAU96338
ID AAU96338 standard; protein; 509 AA.
XX
AC AAU96338;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #25.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69583.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 139-141; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 509 AA;

Query Match 81.8%; Score 2542; DB 5; Length 509;
Best Local Similarity 81.7%; Pred. No. 2.6e-176;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

```
Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||| :|:  | ||||||||: |||||:||||||||||||||||||||||||||||||||
Db          1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
```

```
Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||| ||
Db        121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||:|||| |||||||||||||||| ||::||||:|||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              |||||||||||||:|||||||||||||||| ||||||||||||||:||:|||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||   || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                 ||||: |||||||||||:|||||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
              || || |       || |
Db        492 DCPKGTRWHATLKNCIQE 509
```

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RESULT 9
AAY52535
ID   AAY52535 standard; protein; 490 AA.
XX
AC   AAY52535;
XX
DT   06-AUG-2003  (revised)
DT   22-FEB-2000  (first entry)
XX
DE   D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490.
XX
KW   Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW   house dust mite; IgE; immunoglobulin E; allergen; mapB;
KW   hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW   canine; veterinary; antibody; vaccine; immunisation.
XX
OS   Dermatophagoides pteronyssinus.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   115. .117
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   240. .242
FT                   /note= "Asn is N-glycosylated"
XX
PN   WO9954349-A2.
XX
PD   28-OCT-1999.
XX
PF   16-APR-1999;   99WO-US008524.
XX
PR   17-APR-1998;   98US-00062013.
PR   13-MAY-1998;   98US-0085295P.
PR   02-SEP-1998;   98US-0098909P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2000-052700/04.
DR   N-PSDB; AAZ38589, AAZ38590.
XX
PT   Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT   used to modify an animals' hypersensitivy to mite allergens.
XX
PS   Claim 3; Page 147-149; 154pp; English.
XX
CC   This sequence represents Dermatophagoides pteronyssius mite allergen
CC   protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490
CC   has a molecular weight of 98 kD, comprising 490 amino acids, and has a
CC   high degree of homology with the D. farinae mature 98 kD allergen, mapB
CC   (AAY52525). Nucleic acid molecules encoding PDerp98-490 were isolated
CC   from a D. pteronyssius cDNA library by hybridisation with a probe
CC   encoding the D. farinae high molecular weight map (HMW-map) composition.
CC   Mite allergenic proteins and peptides, and nucleic acids encoding them,
CC   may be used in therapeutic compositions to modify an animal's
CC   hypersensitivity reaction to mite allergens. Animals that may be treated
CC   include mammals and birds, especially felines, canines, equines, humans,
CC   other pets, and work or domestic animals. The proteins or fragments may
CC   also be used to diagnose allergies via a skin test. The proteins and
CC   peptides can also be used to raise antibodies, which have a variety of
CC   potential uses. For example, they can be used as vaccines to passively
CC   immunise animals against dust mite hypersensitivity, as positive controls
CC   in test kits and as tools to recover desired dust mite allergens from a
CC   mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 490 AA;
```

```
  Query Match             79.7%;  Score 2475;  DB 3;  Length 490;
  Best Local Similarity   82.5%;  Pred. No. 1.9e-171;
  Matches  443;  Conservative   21;  Mismatches   21;  Indels   52;  Gaps    2;

Qy         22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 81
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 62

Qy         82 DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
              ||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||:|
Db         63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122

Qy        142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
              |||||||||||||||||||||||||||||||||||| ||||||:|||| ||||||||||
Db        123 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG 182

Qy        202 KDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
              ||||| ||::||||:|||||||||||||||||| :|||||||||||||||||||||||||
Db        183 KDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 242

Qy        262 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 321
              |||||||||||||||||||||||||||||||:||||||||||||||:||||||||||||
Db        243 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 302

Qy        322 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 381
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        303 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362

Qy        382 DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTP 441
              |||||||| |||||||||||||||:||:||||||||||   || |||||
Db        363 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTPTTPSTTSTTTPT------- 415

Qy        442 TTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVD 501
                                                  ||||: |||||||||:|
Db        416 ----------------------------------------PTTTDSTSETPKYTTYID 433

Qy        502 GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 555
              ||||||||:| :||||::|||||||::   ||||||||| || || |      || |
Db        434 GHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIMDCPKGTRWHATLKNCIQE 490
```

```
RESULT 10
AAU96339
ID   AAU96339 standard; protein; 490 AA.
XX
AC   AAU96339;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Der HMW-map polypeptide #26.
XX
KW   Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW   mite allergenic protein; immunoglobulin E; hypersensitivity;
KW   immunocomplex formation.
XX
OS   Dermatophagoides farinae.
XX
PN   WO200222807-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028730.
XX
PR   14-SEP-2000; 2000US-00662293.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2002-351888/38.
DR   N-PSDB; ABK69585.
XX
PT   New mite allergenic protein isolated from Dermatophagoides, designated
PT   Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS   Claim 12; Page 144-146; 161pp; English.
XX
CC   The invention relates to an isolated mite allergenic protein of
CC   Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC   acid. The Der HMW-map protein is useful for eliciting an immune response
CC   against Der HMW-map protein. The protein or a reagent comprising a non-
CC   proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC   cat) susceptible to or having an allergic response to a mite. A
CC   therapeutic composition is useful for desensitising a host animal to an
CC   allergic response to a mite. The DNA and protein can be used in the
CC   detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC   of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC   disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC   binding of proteins to IgE, to prevent immunocomplex formation, thus
CC   reducing hypersensitivity responses to mite allergens, and as vaccines
CC   against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC   represent Der HMW-map polypeptides of the invention
XX
SQ   Sequence 490 AA;

  Query Match             79.7%;  Score 2475;  DB 5;  Length 490;
  Best Local Similarity   82.5%;  Pred. No. 1.9e-171;
  Matches  443;  Conservative   21;  Mismatches   21;  Indels   52;  Gaps    2;

Qy         22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 81
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 62

Qy         82 DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
              ||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||:|
Db         63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122

Qy        142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
              |||||||||||||||||||||||||||||||||| ||||||:|||| ||||||||||
Db        123 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG 182

Qy        202 KDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
              ||||| ||::||||:|||||||||||||||| :|||||||||||||||||||||||||
Db        183 KDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 242

Qy        262 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 321
              |||||||||||||||||||||||||||||||||:|||||||||||||||:||||||||||
Db        243 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 302

Qy        322 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        303 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362

Qy        382 DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTTPTTTPTTPSPTTP 441
              ||||||||| |||||||||||||||:||:||||||||||||  || |||||
Db        363 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTPTTPSTTSTTTPT------- 415

Qy        442 TTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVD 501
                                                          ||||: ||||||||||:|
Db        416 ----------------------------------------PTTTDSTSETPKYTTYID 433

Qy        502 GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 555
              ||||||||:| :||||::||||||::   |||||||| || || |      || |
Db        434 GHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIMDCPKGTRWHATLKNCIQE 490


RESULT 11
ABP72636
ID   ABP72636 standard; protein; 525 AA.
XX
AC   ABP72636;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Anopheles gambiae chitinase.
XX
KW   Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
KW   neuropeptide; transgenic plant; crop protection; mosquito.
XX
OS   Anopheles gambiae.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .525
FT                   /label= Mature_protein
FT   Misc-difference 31
FT                   /note= "possible trypsin activation site"
FT   Misc-difference 32
FT                   /note= "possible trypsin activation site"
FT   Active-site     150. .157
FT   Domain          401. .466
FT                   /note= "serine/threonine/proline-rich domain"
XX
PN   WO2003014150-A2.
XX
PD   20-FEB-2003.
XX
PF   06-AUG-2002; 2002WO-GB003598.
XX
PR   08-AUG-2001; 2001GB-00019274.
XX
PA   (UYDU-) UNIV DURHAM.
PA   (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
XX
PI   Gatehouse JA,  Fitches EC,  Edwards JP;
XX
DR   WPI; 2003-278469/27.
DR   N-PSDB; ABZ81875.
XX
PT   Fusion protein useful for combating insect pests, comprises a
PT   translocating moiety comprising a plant protein capable of acting as a
PT   carrier to translocate toxic moiety inside plant pathogen, and a toxic
PT   moiety.
XX
PS   Claim 7; Fig 15; 51pp; English.
XX
```

CC The present sequence is that of the mosquito Anopheles gambiae chitinase.
CC This protein is used in claimed fusion proteins of the invention. Such
CC fusion proteins comprise a translocating moiety and a toxic moiety, where
CC the translocating moiety is a plant protein (e.g. a lectin) capable of
CC acting as a carrier to translocate the toxic moiety across the gut wall
CC of a plant pathogen, and the toxic moiety is an insect-derived peptide or
CC protein capable of causing deleterious effects on growth, development,
CC reproduction or mortality in pest insects. Suitable insect peptides and
CC proteins include allatostatins, chitinase, diuretic hormone and their
CC metabolites and analogues. Polynucleotides encoding the fusion protein,
CC vectors, host cells and transgenic plants that are resistant to disease
CC are also provided. The fusion protein is target-specific, and resists
CC degradation in the insect gut
XX
SQ Sequence 525 AA;

Query Match 32.5%; Score 1008.5; DB 6; Length 525;
Best Local Similarity 38.4%; Pred. No. 1.1e-64;
Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

```
Qy          8 LSIMACIGLMNASIKRD-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM 65
              : ::  : :  |:   : |   |    ::|||||||:||   :  | || |||  |||||
Db          5 VGVLVLVAVAAAAFAEEPHKAASAEGKKVVCYVGTWAVYRPGNGRYDIEHIDPSLCTHLM 64

Qy         66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125
              |||  |:|   |::: ||| |   | | :  :||  |:   | | |: ::||| ||| |
Db         65 YGFFGINE-DATVRIIDPYLDLEEN-WGRGHIKRFVGLKNVGPGLKTLAAIGGWNEGSRK 122

Qy        126 YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKD 185
             :| |||:   |::||   : | | : |||:|||||||  | ||| ||: |:  || |:::
Db        123 FSAMAASGELRKRFISDCVAFCQRHGFDGIDLDWEYPAQRDGNPLIDRDNHAQLVEEMRE 182

Qy        186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245
              |: :| ||||||:  :     :|||  ::| | ::||| || || |::: | |||||:
Db        183 EFDHYGLLLTAAVASVEFSAGVSYDIPRISKSFHFLNVMVYDMHGAWDSYCGINAPLYRG 242

Qy        246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
               :| :     ||| ::|::|  | |  |||:|:| ||| :::   :  ::| |  |
Db        243 SADTTDRLGQINVNASIHFWLAQGCTGRKLVLGIPLYGRNFTLASAANTQIGAPTVGGGT 302

Qy        306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL 365
              |  : | ||: | | |:    | | ::: |    ||   :  ||||||| |:  |: :|
Db        303 VGRYTREPGVMGYNEFCEKLATEAWDLRWSEEQQVPYAVRNNQWVGYDDLRSVQLKVKYL 362

Qy        366 KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTT 424
              : |: | |||||| ||| | | | : ||:::: :::||           |||||  |:
Db        363 LDQGLGGAMVWSLETDDFLGVCGGGRYPLMHEIRSLVNGGT---------PSTTTMPPSV 413

Qy        425 TPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSP 484
              |||     :| :| | ||||:   | ||  ||  :  |: || : ||     ||  ||
Db        414 APTT-----STVAPGTTTTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG 466

Qy        485 TTTEHTSETPKYTTYVDGHLIKCY--KEGDIPHPTNIHKYLVC-------EFVNGGWWVH 535
                            ||    :  | :|||||  :| :|       ||
Db        467 ----------------DG---PCAGGRYGFVPHPTNCARYYICLTADTYYEFT------- 500

Qy        536 IMPCPPGTIW 545
                |||||::
Db        501 ---CPPGTLF 507
```

RESULT 12
ABB58595
ID ABB58595 standard; protein; 4498 AA.
XX
AC ABB58595;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 2577.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL02698.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 2577; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4498 AA;

Query Match 27.5%; Score 854.5; DB 4; Length 4498;
Best Local Similarity 33.8%; Pred. No. 2.8e-52;
Matches 202; Conservative 88; Mismatches 188; Indels 119; Gaps 21;

```
Qy          2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID 57
              :|:: : ::  ||           |: |    |:|||   ||||     | :|   ::|:
Db         33 QTLFLLCALAYCI----------NEASSEG-RVVCYYTNWSVYRPGTAKFNP---QNIN 77

Qy         58 PFKCTHLMY---GFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMI 114
              |: ||||:|   || | :: |     || |||       |: || :|  |:  | :| |||
Db         78 PYLCTHLVYAFGGFTKDNQMK----PFDKYQD-----IEQGGYAKFTGLKTYNKQLKTMI 128

Qy        115 SLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQ 174
              ::||| | | ::| : |:   |||||:::| ||::  |||:|||||||  | |     |:
Db        129 AIGGWNEASSRFSPLVASNERRQQFIKNILKFLRQNHFDGIDLDWEYPAHREGGKSRDRD 188

Qy        175 NYLALVRELKDAFEPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYD 227
              ||   |:||:  ||            ||| ||  | : ||: ||: :|||  || ||:|||
Db        189 NYAQFVQELRAEFEREAEKTGRTRLLLTMAVPAGIEYIDKGYDVPKLNKYLDWFNVLTYD 248

Qy        228 YHGGWENFYGHNAPLYKRPDETDELHTY---FNVNYTMHYYLNNGATRDKLVMGVPFYGR 284
              :|   |    |:||||    | |  : |    |::|:: |||  || |||||:|:| |||
Db        249 FHSSHEPSVNHHAPLYSL--EEDSEYNYDAELNIDYSIKYYLKAGADRDKLVLGIPTYGR 306

Qy        285 AWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE-EWH-IQYDEYYNAPY 342
              :::: :    :|| ||:|    |  : |:| |:| |:||  : : ||  :| :      ||
Db        307 SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY 366

Qy        343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMI 401
              |    |||||| | :  |  ::   |: |:| |:::||||:| | |   ||:
Db        367 AYRRNQWVGYDDEAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIEAA---- 422

Qy        402 NGDEKNSFECILGPSTTTPTPTTTPTTTPTTTPT-------------TPSPTT---PTTTP 445
                  | :    ||       : |  |: : :                | :| :    |: |
Db        423 ----KEAMVEALGLGINEVAKPSGPQKPSRSRSRDNASNRNRLNGKTEAPLSSRRPSATR 478
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Qy        446 SPTTPTTTPSPTTPTTT----------------PSPTTPTPTTPTPAPTTSTPSPTTTEH 489
Db        479 RPAVSSTQAPP--PSTTFKLTEAEGSSLYIGGRASTTPPPPTTPDP-------------- 522

Qy        490 TSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNG----GWWVHIMPCPPG 542
Db        523 -----------GSDFKCEEEGFFQHPRDCKKYYWC-LDSGPSGLGIVAHMFTCPSG 566


RESULT 13
AAW01824
ID   AAW01824 standard; protein; 554 AA.
XX
AC   AAW01824;
XX
DT   27-MAY-1997  (first entry)
XX
DE   Manduca sexta larva epidermal and gut chitinase.
XX
KW   Chitinase; insect; transgenic plant; biological control; baculovirus;
KW   biocide; insecticide; tobacco hookworm.
XX
OS   Manduca sexta.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Sig_peptide
FT   Protein         20. .554
FT                   /label= Mat_protein
FT   Region          97. .111
FT                   /label= Conserved_region-I
FT   Active-site     136. .148
FT                   /note= "proposed active site"
XX
PN   WO9708944-A1.
XX
PD   13-MAR-1997.
XX
PF   06-SEP-1996;   96WO-US014440.
XX
PR   06-SEP-1995;   95US-00524051.
XX
PA   (UNIV ) UNIV KANSAS STATE RES FOUND.
XX
PI   Kramer KJ,  Muthukrishnan S,  Choi HK,  Corpuz L,  Gopalakrishnan B;
XX
DR   WPI; 1997-192586/17.
DR   N-PSDB; AAT62557.
XX
PT   Transgenic plant contg. recombinant insect chitinase coding sequence -
PT   useful for controlling plant pests.
XX
PS   Claim 4; Page 37-40; 57pp; English.
XX
CC   An epidermal and gut chitinase (AAW01824) of Manduca sexta is encoded by
CC   cDNA clone 201 (AAT62557), isolated from a day-6 fifth instar whole larva
CC   cDNA library. The cDNA can be inserted into a vector for host expression
CC   of the chitinase protein, and may be utilised to control a population of
CC   insect pests. A recombinant baculovirus vector is provided for this
CC   purpose, as well as a transgenic tobacco plant that shows increased
CC   resistance to tobacco hornworm. Recombinant chitinase may also be
CC   expressed in host cells or larvae for subsequent purification and use as
CC   a biocide. The insect chitinase is expected to be more potent as an
CC   insect control agent than chitinases from other sources
XX
SQ   Sequence 554 AA;

  Query Match             27.0%;  Score 838.5;  DB 2;  Length 554;
  Best Local Similarity   35.4%;  Pred. No. 2.8e-52;
  Matches  208;  Conservative   79;  Mismatches  210;  Indels   91;  Gaps   20;

Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64

Db          3 ATLATLAVLALATAV-------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI 55

Qy         65 MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE 124
Db         56 IYSFIGVTEGNSEVLIIDPELD-----VDKNGFRNFTSLRSSHPSVKFMVAVGGWAEGSS 110

Qy        125 KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
Db        111 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDWEYPGAADRGGSPSDKDKFLYLVQEL 170

Qy        184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241
Db        171 RRAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP 230

Qy        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED---------- 290
Db        231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI 289

Qy        291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
Db        290 NKEAGGGDPAPYTNATGF-------WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342

Qy        349 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
Db        343 WVGYEDPRSVEIKMNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS------ 396

Qy        409 FECILGPSTTTPTPTTTPTTPT-------TTPTTPS-----PTTPTTTPSPTTPTTTPSP 456
Db        397 -------SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTTTAKPASTTKTTVKTT 449

Qy        457 TTPTTTPSPTT----------PTP-TTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI 505
Db        450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE----------VDGSEI 497

Qy        506 KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
Db        498 -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540


RESULT 14
AAB07183
ID   AAB07183 standard; protein; 554 AA.
XX
AC   AAB07183;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Manduca sexta gut chitinase.
XX
KW   Imaginal disc growth factor; IDGF; chitinase related protein; CHRP;
KW   tissue growth; wound healing; bone repair; cartilage repair;
KW   angiogenesis; meat production; milk production; cancer; gene therapy;
KW   gut chitinase.
XX
OS   Manduca sexta.
XX
PN   US6060590-A.
XX
PD   09-MAY-2000.
XX
PF   31-MAR-1998;   98US-00052778.
XX
PR   31-MAR-1998;   98US-00052778.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Bryant PJ,  Kawamura K;
XX
DR   WPI; 2000-349702/30.
XX
PT   New imaginal disc growth factor polypeptide, useful for healing wounds,
PT   promoting tissue growth, modulating female reproductive tract functions
```

PT and treating cell proliferative disorders such as cancer and metastasis.
XX
PS Disclosure; Col 53-58; 40pp; English.
XX
CC The present sequence is the protein sequence for the Manduca sexta gut
CC chitinase. It was used to isolate the Drosophila melanogaster imaginal
CC disc growth factor 4 (IDGF4) coding sequence. IDGF4 is a member of the
CC chitinase related proteins (CHRP) and is involved in the promotion of
CC cell growth, motility and morphogenesis. The gene and protein are
CC expected to have mammalian homologues. They can be used in the treatment
CC of cancer, wound healing, tissue regeneration following arthritis,
CC osteoporosis, other skeletal disorders and burns, for revitalising scar
CC tissue resulting from surgical procedures, irradiation, laceration, toxic
CC chemicals, viral or bacterial infection or burns, to promote tissue
CC growth during tissue engineering, for example tissues for skin graft
CC replacements and bone regrowth, and to modulate the function of the
CC female reproductive tract. In addition, they can also be used to increase
CC meat, egg, sperm and milk production in animals. One possible method of
CC use is by gene therapy
XX
SQ Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 3; Length 554;
Best Local Similarity 35.4%; Pred. No. 2.8e-52;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

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Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
              | |: :| : |  |         | :  |||||   |:||   |  | ||||   ||||:
Db          3 ATLATLAVLALATAV-------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI 55

Qy         65 MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE 124
             :| |  : |    : : ||  |      :| |:  | :||  :| :  |:::||| |||
Db         56 IYSFIGVTEGNSEVLIIDPELD-----VDKNGFRNFTSLRSSHPSVKFMVAVGGWAEGSS 110

Qy        125 KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
              ||| | |  : |  ||:||: ||::| |||||||||||:   |    ||  :| ||:||
Db        111 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQEL 170

Qy        184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241
              : ||     |: |||||     ::   | : || :  | ::||:||  | |  |   ::|
Db        171 RRAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP 230

Qy        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED---------- 290
              ||||| :    :   |||  :| :   |   :|||:|:|||||::::
Db        231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI 289

Qy        291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
              :   ||||   :  ||      :| |:|    |::  |  ::||    || |
Db        290 NKEAGGGDPAPYTNATGF-------WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342

Qy        349 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
              ||||:|  |:  |: ::|: |  | | |::: |||:| || ||||:  :|  ::
Db        343 WVGYEDPRSVEIKMNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS------ 396

Qy        409 FECILGPSTTTPTPTTTPTTPT-------TTPTTPS-----PTTPTTTPSPTTPTTTPSP 456
                  | | | |  |||       :||: ||     ||| |  |: || ||  :
Db        397 -------SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTTAKPASTTKTTVKTT 449

Qy        457 TTPTTTPSPTT----------PTP-TTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI 505
              || |  |  :          | |  | | |  | ||  |           |||  |
Db        450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE----------VDGSEI 497

Qy        506 KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
               |  : | ||   :  ||  |  |||        |  ||::  |   |
Db        498 -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540
```

RESULT 15
ABP72619
ID ABP72619 standard; protein; 554 AA.
XX
AC ABP72619;
XX
DT 11-JUN-2003 (first entry)
XX
DE Manduca sexta chitinase.
XX
KW Insecticide; pesticide; insect control; insect; toxin; chitinase; enzyme;
KW neuropeptide; transgenic plant; crop protection.
XX
OS Manduca sexta.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .19
FT		/label= Signal_peptide
FT	Protein	20. .554
FT		/label= Mature_protein
FT	Modified-site	85. .88
FT		/note= "Asn is N-glycosylated"
FT	Active-site	138. .146
FT	Modified-site	303. .306
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	545. .548
FT		/note= "Asn is N-glycosylated"

XX
PN WO2003014150-A2.
XX
PD 20-FEB-2003.
XX
PF 06-AUG-2002; 2002WO-GB003598.
XX
PR 08-AUG-2001; 2001GB-00019274.
XX
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
XX
PI Gatehouse JA, Fitches EC, Edwards JP;
XX
DR WPI; 2003-278469/27.
XX
PT Fusion protein useful for combating insect pests, comprises a
PT translocating moiety comprising a plant protein capable of acting as a
PT carrier to translocate toxic moiety inside plant pathogen, and a toxic
PT moiety.
XX
PS Claim 7; Fig 10; 51pp; English.
XX
CC The present sequence is that of Manduca sexta chitinase. This protein can
CC be used in claimed fusion proteins of the invention. Such fusion proteins
CC comprise a translocating moiety and a toxic moiety, where the
CC translocating moiety is a plant protein (e.g. a lectin) capable of acting
CC as a carrier to translocate the toxic moiety across the gut wall of a
CC plant pathogen, and the toxic moiety is an insect-derived peptide or
CC protein capable of causing deleterious effects on growth, development,
CC reproduction or mortality in pest insects. Suitable insect peptides and
CC proteins include allatostatins, chitinase, diuretic hormone and their
CC metabolites and analogues. Polynucleotides encoding the fusion protein,
CC vectors, host cells and transgenic plants that are resistant to disease
CC are also provided. The fusion protein is target-specific, and resists
CC degradation in the insect gut
XX
SQ Sequence 554 AA;

Query Match 27.0%; Score 838.5; DB 6; Length 554;
Best Local Similarity 35.4%; Pred. No. 2.8e-52;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

```
Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
              | |: :| : |  |         | :  |||||   |:||   |  | ||||   ||||:
Db          3 ATLATLAVLALATAV-------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI 55

Qy         65 MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE 124
             :| |  : |    : : ||  |      :| |:  | :||  :| :  |:::||| |||
Db         56 IYSFIGVTEGNSEVLIIDPELD-----VDKNGFRNFTSLRSSHPSVKFMVAVGGWAEGSS 110

Qy        125 KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
```

```
                ||| | |  : |  ||:||: ||::| ||||||||||||:   |    ||  :| ||:||
Db        111 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQEL 170

Qy        184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241
                : ||     |: |||||     ::   | : || :  | ::||:||  | |  |   ::|
Db        171 RRAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP 230

Qy        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED---------- 290
                ||||| :    :   |||  :| :   |   :|||:|:|||||::::
Db        231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI 289

Qy        291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
                :   ||||   :  ||        :| |:|    |::  |  ::||    || |
Db        290 NKEAGGGDPAPYTNATGF-------WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342

Qy        349 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
                ||||:|  |:  |: ::|: |  | | |::: |||:| || ||||:  :|  ::
Db        343 WVGYEDPRSVEIKMNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS------ 396

Qy        409 FECILGPSTTTPTPTTTPTTPT-------TTPTTPS-----PTTPTTTPSPTTPTTTPSP 456
                      | | | | |  ||||       :||: ||     ||| |  |: || ||  :
Db        397 -------SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTTAKPASTTKTTVKTT 449

Qy        457 TTPTTTPSPTT----------PTP-TTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI 505
                || |  |  :          | |   | | |    | ||  |             |||  |
Db        450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE----------VDGSEI 497

Qy        506 KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
                 |  : | ||   :  ||  |  |||       |  ||::  |   |
Db        498 -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540
```

Search completed: March 31, 2006, 15:04:01
Job time : 198 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:04:19 ; Search time 41 Seconds
(without alignments)
1302.446 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1008.5	32.5	525	2	T44445	chitinase (EC 3.2.
2	869	28.0	1635	2	T14075	chitinase (EC 3.2.
3	838.5	27.0	554	2	A56596	chitinase (EC 3.2.
4	825.5	26.6	588	2	JC8021	chitinase (EC 3.2.
5	802	25.8	483	2	A53918	chitinase (EC 3.2.
6	705.5	22.7	617	2	T15408	hypothetical prote
7	685.5	22.1	537	2	S57197	oviduct-specific g
8	685	22.0	539	2	I46470	estrogen dependent
9	668	21.5	654	2	I38605	oviductal glycopro
10	662	21.3	383	2	A49562	cartilage glycopro
11	650	20.9	383	2	S51327	heparin-binding gl
12	646.5	20.8	405	2	S61551	breast-regressing
13	608	19.6	399	2	S27879	secretory protein
14	604.5	19.5	504	2	A38221	chitinase (EC 3.2.
15	592	19.1	599	2	D83764	chitinase BH0916 [
16	561	18.1	699	2	A38368	chitinase (EC 3.2.
17	560	18.0	1215	2	T43916	chitinase A [impor
18	463.5	14.9	831	2	T00323	chitinase (EC 3.2.
19	432.5	13.9	1484	2	T29275	hypothetical prote
20	428	13.8	869	2	T44440	chitinase (EC 3.2.
21	427.5	13.8	849	2	D82510	chitinase VCA0027
22	424.5	13.7	2025	2	T03884	hypothetical prote
23	414.5	13.3	563	2	S60651	chitinase precurso
24	413	13.3	756	2	AB1452	chitinase B homolo
25	412	13.3	423	2	JQ1975	chitinase (EC 3.2.
26	411.5	13.2	424	2	S68121	chitinase I precur
27	411	13.2	423	2	S51369	chitinase - fungus
28	409.5	13.2	756	2	AB1088	chitinase B homolo
29	408.5	13.1	561	2	A25090	chitinase (EC 3.2.
30	405	13.0	546	2	F84238	chitinase [importe
31	394	12.7	452	2	JC4038	47K glycoprotein p
32	394	12.7	633	2	T24898	hypothetical prote
33	391.5	12.6	558	2	T30418	chitinase (EC 3.2.
34	389	12.5	424	2	S47133	chitinase (EC 3.2.
35	388	12.5	820	2	A40633	chitinase (EC 3.2.
36	385	12.4	799	2	PC4106	chitinase (EC 3.2.
37	382	12.3	755	2	T20950	hypothetical prote
38	379.5	12.2	765	2	T35719	chitinase - Strept
39	377.5	12.1	550	2	T10393	chitinase (EC 3.2.
40	371.5	12.0	398	2	T04761	chitinase homolog
41	369	11.9	1088	2	D82246	probable chitinase
42	367.5	11.8	511	2	S61166	probable membrane
43	365	11.7	379	2	T04762	chitinase homolog
44	364.5	11.7	552	2	T41863	chitinase chi-A or
45	360.5	11.6	551	2	G72865	chitinase - Autogr

ALIGNMENTS

RESULT 1
T44445
chitinase (EC 3.2.1.14) [imported] - African malaria mosquito
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44445
R;Shen, Z.; Jacobs-Lorena, M.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z22771
A;Accession: T44445
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-525 <SHE>
A;Cross-references: UNIPROT:O44079; UNIPARC:UPI0000079CC9; EMBL:AF008575; PIDN:AAB8776
A;Experimental source: adult; gut
C;Genetics:
A;Gene: chi-1
C;Keywords: glycosidase; hydrolase

Query Match 32.5%; Score 1008.5; DB 2; Length 525;
Best Local Similarity 38.4%; Pred. No. 5.5e-55;
Matches 211; Conservative 93; Mismatches 187; Indels 59; Gaps 13;

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Qy          8 LSIMACIGLMNASIKRD-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM 65
              : ::  : :  |:   : |   |    ::|||||||:||   :  | || |||  |||||
Db          5 VGVLVLVAVAAAAFAEEPHKAASAEGKKVVCYVGTWAVYRPGNGRYDIEHIDPSLCTHLM 64

Qy         66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125
              |||  |:|   |::: ||| |   | | :  :||  |:   | | |: ::||| ||| |
Db         65 YGFFGINE-DATVRIIDPYLDLEEN-WGRGHIKRFVGLKNVGPGLKTLAAIGGWNEGSRK 122

Qy        126 YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKD 185
             :| |||:   |::||   : | | : |||:|||||||  | ||| ||: |:  || |:::
Db        123 FSAMAASGELRKRFISDCVAFCQRHGFDGIDLDWEYPAQRDGNPLIDRDNHAQLVEEMRE 182

Qy        186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245
              |: :| ||||||:  :     :|||  ::| | ::||| || || |::: | |||||:
Db        183 EFDHYGLLLTAAVASVEFSAGVSYDIPRISKSFHFLNVMVYDMHGAWDSYCGINAPLYRG 242

Qy        246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
              :| :     ||| ::|::|  | |  |||:|:| ||| :::   :  ::| | |
Db        243 SADTTDRLGQINVNASIHFWLAQGCTGRKLVLGIPLYGRNFTLASAANTQIGAPTVGGGT 302

Qy        306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL 365
              |  : | ||: | | |:    | | ::: |    ||   :  |||||| |:  |: :|
Db        303 VGRYTREPGVMGYNEFCEKLATEAWDLRWSEEQQVPYAVRNNQWVGYDDLRSVQLKVKYL 362

Qy        366 KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSPECILGPSTTTPTPTT 424
              : |: | ||||||| ||| | | | : ||:::: :::||           |||||  |:
Db        363 LDQGLGGAMVWSLETDDFLGVCGGGRYPLMHEIRSLVNGGT---------PSTTTMPPSV 413

Qy        425 TPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSP 484
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```
Db        414 APTT-----STVAPGTTTTTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG 466

Qy        485 TTTEHTSETPKYTTYVDGHLIKCY--KEGDIPHPTNIHKYLVC-------EFVNGGWWVH 535

Db        467 ----------------DG---PCAGGRYGFVPHPTNCARYYICLTADTYYEFT------- 500

Qy        536 IMPCPPGTIW 545

Db        501 ---CPPGTLF 507
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RESULT 2
T14075
chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14075
R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A;Reference number: Z17872
A;Accession: T14075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1635 <DEL>
A;Cross-references: UNIPROT:O17412; UNIPARC:UPI000008366A; EMBL:AF026492; NID:g2564720;
C;Genetics:
A;Gene: CHT2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.0%; Score 869; DB 2; Length 1635;
Best Local Similarity 34.3%; Pred. No. 1e-45;
Matches 196; Conservative 95; Mismatches 196; Indels 84; Gaps 18;

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Qy         21 IKRDHNDYSKNPM------RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDE 73

Db        650 INKETSNQDENAIESDVDYKVVCYFTNWAWYRQGNGKYLPEDIDADLCTHIVYGFAVLDR 709

Qy         74 YKYTIQVFDPYQDDNHNSW---EKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDM 129

Db        710 DRLVIK--------PHDSWADIDNRFYERVVEYKKKGKKVT--VAIGGWNDSAGDKYSRL 759

Qy        130 AANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPK----IDKQNYLALVRELKD 185

Db        760 VRSAAARQKFIADVVAFIEKYGFDGLDLDWEYPVCWQVDCKKGFSDEKEGFASLVVELSQ 819

Qy        186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245

Db        820 AFKPKGLLLSSAVSPSKKVVDEGYDVVTLSDYMDWIAVMAYDYHGQWDKKTGHVAPMYEH 879

Qy        246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305

Db        880 PDDFDKT---FNANFTIHYWIEKGADPRKLVMGMPMYGQSFSLADNKEHGLNAKTYGGGE 936

Qy        306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAF 364

Db        937 AGESTRARGFLSYYEICANIRNKKWTVARDRKGRMGPYAYKGDQWVSFDDQYMIRHKSEY 996

Qy        365 LKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECIL--GPSTTTPT 421

Db        997 VKAMGLGGAMIWALDLDDFRNLCDCEEYPLLRTINRVLRNYPGPGPRCVLEKEPQREEPR 1056

Qy        422 PTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTST 481

Db       1057 PTRPPTS----------TTPETTRRPSTTTSTRRTTMTTTT--TTTRRPTTTTRRRTSAR 1104

Qy        482 PSPTTTEHTSETPKY---------TTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGW 532

Db       1105 PTYTTT----NVPSYQEIANEVDEPTCTDGRLF-------VPHPTDCNKYYICQYGK--- 1150

Qy        533 WVHIMPCPPGTIW-----------CQEKLT 551

Db       1151 -----LCPGGLYWSVDHCDWPQSTNCRNKQT 1176
```

RESULT 3
A56596
chitinase (EC 3.2.1.14) - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: A56596
R;Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S.
Insect Biochem. Mol. Biol. 23, 691-701, 1993
A;Title: Sequence of a cDNA and expression of the gene encoding epidermal and gut chiti
A;Reference number: A56596; MUID:93357793; PMID:8353525
A;Accession: A56596
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <KRA>
A;Cross-references: UNIPROT:P36362; UNIPARC:UPI0000127829; GB:U02270; GB:S64757; NID:g4
A;Experimental source: larvae
A;Note: sequence extracted from NCBI backbone (NCBIN:136417, NCBIP:136418)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 1.9e-44;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;

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Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64

Db          3 ATLATLAVLALATAV-------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI 55

Qy         65 MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE 124

Db         56 IYSFIGVTEGNSEVLIIDPELD-----VDKNGFRNFTSLRSSHPSVKFMVAVGGWAEGSS 110

Qy        125 KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183

Db        111 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQEL 170

Qy        184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241

Db        171 RRAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP 230

Qy        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----------- 290

Db        231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI 289

Qy        291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348

Db        290 NKEAGGGDPAPYTNATGF-------WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342

Qy        349 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408

Db        343 WVGYEDPRSVEIKMNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS------ 396

Qy        409 FECILGPSTTTPTPTTTPTTPT-------TTPTTPS-----PTTPTTTPSPTTPTTTPSP 456

Db        397 -------SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTTAKPASTTKTTVKTT 449

Qy        457 TTPTTTPSPTT----------PTP-TTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI 505

Db        450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE----------VDGSEI 497

Qy        506 KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552

Db        498 -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540
```

RESULT 4
JC8021
chitinase (EC 3.2.1.14) - Helicoverpa armigera
C;Species: Helicoverpa armigera
C;Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004

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C;Accession: JC8021
R;Ahmad, T.; Rajagopal, R.; Bhatnagar, R.K.
Biochem. Biophys. Res. Commun. 310, 188-195, 2003
A;Title: Molecular characterization of chitinase from polyphagous pest Helicoverpa armig
A;Reference number: JC8021; PMID: 14511669
A;Accession: JC8021
A;Molecule type: mRNA
A;Residues: 1-588 <AHM>
A;Cross-references: GB:AY325496/AY326455
C;Comment: This enzyme belongs to the family 18 glycosyl hydrolases and plays protective
 and metabolism; in higher vertebrates it is produced as an immune response towards fung
C;Keywords: chitinase; glycosylated protein

  Query Match             26.6%;  Score 825.5;  DB 2;  Length 588;
  Best Local Similarity   34.4%;  Pred. No. 1.3e-43;
  Matches  206;  Conservative   79;  Mismatches  219;  Indels   95;  Gaps   20;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPF 59
              |: | | |:::|   :   :|: |       :  |||||   |:||   |  | ||||
Db          1 MRVILATLAVLA---VATTAIEAD------SKARIVCYFSNWAVYRPGVGRYGIEDIPVD 51

Qy         60 KCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGW 119
               |||::| |  : |    : : ||  |       :| |:  |  ||  :| :   :::|||
Db         52 LCTHIIYSFIGVTEKSNEVLIIDPELD-----VDKNGFRNFTALRKSHPNVKFTVAVGGW 106

Qy        120 YEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLA 178
              ||  ||| | |     |  |::||:|||::| ||||||||||||:   |    ||  :|
Db        107 AEGGSKYSHMVAQKQTRMAFVRSVVDFLKKYDFDGLDLDWEYPGAADRGGSFSDKDRFLF 166

Qy        179 LVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFY 236
              ||:||: ||  |  |: |||||     ::   |   :| :  | ::||:|| | |  |
Db        167 LVQELRRAFIREKRGWELTAAVPLANFRLMEGYHCPDLCQELDAIHVMSYDLRGNWAGFA 226

Qy        237 GHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED------ 290
                ::|||||| :    :   |||  :  :   |   :|||:|:|||||:::: 
Db        227 DVHSPLYKRPHD-QWAYEKLNVNDGLALWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYG 285

Qy        291 -----RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPYG 343
                   :   ||||   :  ||        :| |:|    ||   |  ::|:    ||
Db        286 LGTYINKEAGGGDPAPYTNATGF-------WAYYEICTEVDKEGSGWTKKWDDAGKCPYA 338

Qy        344 YNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMING 403
              |    ||||:|  |:  |: ::|| |  | | |::: ||||| || :|||:  :|  ::
Db        339 YKGTQWVGYEDPRSVEIKMNWIKEKGYLGAMTWAIDMDDFKGLCGDENPLIKLLHKHMS- 397

Qy        404 DEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTT------------PTTTPSPTTP 450
                      : | | :  ||||      |  ||               |||    ||
Db        398 -----------TYTVPPPRSGNTTPTPEWARPPSTTSDPAEGEIVTTVKPTTAKPATTK 445

Qy        451 TTTPSPTT-PTTTPSPTTPTPTTPTPAPTTST-----------PSPTTTEHTSETP---- 494
              ||  |||   ||  |||  ||| | ||  |           | |     | |||
Db        446 PTTAKPTTAKPTTAKPTTAKPTT-TKAPQVVTIPDDENDIAVRPEPPKKPVTPETPVVPE 504

Qy        495 -------KYTTYVDGHLIKCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIW 545
                    :| | : |  | | :|      ||  |  |||     :  | |||::
Db        505 VPESAETPTENEIDNHDV-CNSEEDYVPDKKKCDKYWRC--VNGQGM--LFTCQPGTVF 558


RESULT 5
A53918
chitinase (EC 3.2.1.14) precursor - braconid wasp (Chelonus sp.)
C;Species: Chelonus sp.
C;Date: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53918
R;Krishnan, A.; Nair, P.N.; Jones, D.
J. Biol. Chem. 269, 20971-20976, 1994
A;Title: Isolation, cloning, and characterization of new chitinase stored in active form
A;Reference number: A53918; MUID:94342256; PMID:8063715
A;Accession: A53918
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-483 <KRI>
A;Cross-references: UNIPROT:Q23737; UNIPARC:UPI0000080E4E; GB:U10422; NID:g533504; PIDN:
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

  Query Match             25.8%;  Score 802;  DB 2;  Length 483;
  Best Local Similarity   36.1%;  Pred. No. 2.9e-42;
  Matches  160;  Conservative   89;  Mismatches  162;  Indels   32;  Gaps    9;

Qy          4 IYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCT 62
              ::  :|::: | :               :| ::||| | |||| : :  : |  |||  ||
Db          6 LFVAISLVSTIAV------------ASPNKVVCYFGAWSVYRQGNGKFDINGIDPTLCT 52

Qy         63 HLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEG 122
              ||:| |  ::     ::| ||: |    |     |: :| :|| ||| :  |:::|||  |
Db         53 HLIYSFVGVN--GKDVKVLDPWSDLPGN---LDGFGKFTSLRKKNPSVKIMVAVGGWNAG 107

Qy        123 SEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRE 182
              |  :| ||::   |: | |:|: |||:|:||| |:|||||  | |:|  | :| : | :
Db        108 SVPFSQMASDQATREAFAQNVVKFLQQYQFDGFDIDWEYPAQRGGSP-ADVKNMVKLCKA 166

Qy        183 LKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYG-HNAP 241
              || ||  | |:|:|||:  :    ::||| |:::  |::|:||||:|| |:   | |  |
Db        167 LKKAFVQHDYILSAAVAAPETSASKSYDIAEMSQYLDFINLMTYDFHGPWDGHTGMHAPP 226

Qy        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAK 301
                |  :||    ||   : |:| ||  ::|||:||| ||::::: : |   || |
Db        227 SASSHDSGNELK--LNVKAAVKYWLQNGVPKEKLVVGVPAYGKSFTLSNPSNKGLGAPVS 284

Qy        302 GMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCK 361
              |    |  :|| |:| | |:|:: :  :| :  |      ||        || :||||:|  |
Db        285 GAGTAGPYTGENGLLGYNEICEMQKAGDWEVVQDNEKGVPYAVKGNQWVSFDDLAAIKAK 344

Qy        362 LAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSPECILGPSTT--- 418
                |:|: |: | ||||:| ||||| || | |:|  :::::      :|       |: |
Db        345 AQFIKQEGLGGAMVWSIETDDFKGLCGEKYPVLKALNSVLGRGGSSS------PAETKRK 398

Qy        419 TPTPTTTPTTPTTTPTTPSPTTP 441
                  |  |  | :     :|  |
Db        399 NNVPDDQPAPPRSFAEDSAPEAP 421


RESULT 6
T15408
hypothetical protein C04F6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15408
R;Nhan, M.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C04F6.
A;Reference number: Z18346
A;Accession: T15408
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-617 <NHA>
A;Cross-references: UNIPROT:Q11174; UNIPARC:UPI0000060EB1; EMBL:U42835; NID:g1125760;
C;Genetics:
A;Gene: CESP:C04F6.3
A;Introns: 28/1; 66/2; 504/1

  Query Match             22.7%;  Score 705.5;  DB 2;  Length 617;
  Best Local Similarity   30.2%;  Pred. No. 3.7e-36;
  Matches  178;  Conservative   90;  Mismatches  210;  Indels  111;  Gaps   19;

Qy         37 CYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKR 95
              ||   |: | :    :  ||  | |||::: |  ::   ||:: :||   |  | |
Db         57 CYFTNWAQYRQGRAKFVPEDYTPGLCTHILFAFGWMNA-DYTVRAYDP--ADLPNDWAGE 113

Qy         96 G-YERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDG 154
              | | | |:: : :| |::| |||  |:  :  |||:   |: || | : |:: : |||
Db        114 GMYRRVNKLKVTDTQLKTLLSFGGWSFGTALFQGMAASSASRKVFIDSAITFVRTWGFDG 173

Qy        155 LDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDKIDR 207
              :|:|||||           | ||:|||:||| | |           |:||||: |   ||
Db        174 IDIDWEYPSG-----ATDMANYVALVKELKAACESEAGSTGKDRLLVTAAVAAGPATIDA 228
```

```
Qy        208 AYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLN 267
Db        229 GYDIPNLAPNFDFILLMSYDFFGAWASLVGFNSPLYATTELPAEWNGW-NVDSSARYWNQ 287

Qy        268 NGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQK 327
Db        288 KGMPKEKIIVGMPTYGRGWTLNNASAINPGTSGSPAKITQYVQ-EAGVGAYFEFCEMLAN 346

Qy        328 EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC 387
Db        347 GATR-YWDSQSQVPYLVQGNQWWSYDDEESFANKMAYVKREGYGGAFVWTLDFDDFNAGC 405

Qy        388 GPKN----PLLNKVHNMINGDEKNSFECIL---GPSTTTPT-----------PTTTPTTP 429
Db        406 SNSNGQLYPLISVIAKELGG-------VIIPKKGGVTTAPTTVATTVTTGRPPMTSAVTT 458

Qy        430 TTTPTTPSPTTPTTTPSPTT---------------------------------------- 449
Db        459 TTAATTTTTRAATTTTASNTNVCSGKSDGFYPNSNNCGLFVLCLSSKSYSMSCPSGLQYS 518

Qy        450 ------PTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGH 503
Db        519 ASLKYCTTSTASGCSVTTTRAPTTTTKSAPT--VTTTTRAPTTT-----TPAF------- 564

Qy        504 LIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
Db        565 --KCTKDGFFGVPSDCLKFIRC--VNG--ISYNFECPNGLSFHADTMMC 607
```

RESULT 7
S57197
oviduct-specific glycoprotein 95K precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57197
R;Sendai, Y.; Abe, H.; Kikuchi, M.; Satoh, T.; Hoshi, H.
Biol. Reprod. 50, 927-934, 1994
A;Title: Purification and molecular cloning of bovine oviduct-specific glycoprotein.
A;Reference number: S57197; MUID:94257768; PMID:8199272
A;Accession: S57197
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-537 <SEN>
A;Cross-references: UNIPROT:Q28042; UNIPARC:UPI0000130C52; EMBL:D16639; NID:g391621; PID
C;Keywords: glycoprotein

  Query Match 22.1%; Score 685.5; DB 2; Length 537;
  Best Local Similarity 33.3%; Pred. No. 5.4e-35;
  Matches 173; Conservative 95; Mismatches 183; Indels 69; Gaps 19;

```
Qy         10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67
Db          1 LLLCVGLL---LVLKHHDGAAH--KLVCYFTNWA-FSRPGPASILPRDLDPFLCTHLVFA 54

Qy         68 FAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYS 127
Db         55 FASMSNNQ--IVPKDP-QD------EKILYPEFNKLKERNRGLKTLLSIGGWNFGTVRFT 105

Qy        128 DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF 187
Db        106 TMLSTFSNRERFVSSVIALLRTHGFDGLDLFFLYPGLR-GSPARDRWTFVFLLEELLQAF 164

Qy        188 EPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
Db        165 KNEAQLTMRPRLLLSAAVSGDPHVVQKAYEARLLGRLLDFISVLSYDLHGSWEKVTGHNS 224

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
Db        225 PLPSLPGDPK------SSAYAMNYWRQLGVPPEKLLMGLPTYGRTFHLLKASQNELRAQA 278

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
```

```
Db        279 VGPASPGKYTKQAGFLAYYEICCFVRRAKKRWINDQY--VPYAFKGKEWVGYDDAISFGY 336

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTT 418
Db        337 KAFFIKREHFGGAMVWTLDLDDFRGYFCGTGPFPLVHTLNNLLVNDEFSS---------- 386

Qy        419 TPTP----TTTPTTPTTTPTTPSPTTPTTTPSPTTP--------TTTPSPTTPTTTPSPT 466
Db        387 TPSPKFWFSTAVNSSRIGPEMPTMTRDLTTGLGILPPGGEAVATETHRKSETMTITPKGE 446

Qy        467 TPTPT-TP------TPAPTTSTPSP-----TTTEHTSETP 494
Db        447 IATPTRTPLSFGRHTAAPEGKTESPGEKPLTTVGHLAVSP 486
```

RESULT 8
I46470
estrogen dependent oviduct protein precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46470
R;DeSouza, M.M.; Murray, M.K.
Endocrinology 136, 2485-2496, 1995
A;Title: An estrogen-dependent secretory protein, which shares identity with chitinases
and embryo development.
A;Reference number: I46470; MUID:95269691; PMID:7750470
A;Accession: I46470
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-539 <DES>
A;Cross-references: UNIPROT:Q28542; UNIPARC:UPI0000130C57; EMBL:U16719; NID:g885600; PI

  Query Match 22.0%; Score 685; DB 2; Length 539;
  Best Local Similarity 33.8%; Pred. No. 5.8e-35;
  Matches 173; Conservative 90; Mismatches 185; Indels 64; Gaps 17;

```
Qy         10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67
Db          4 LLLWVGLL---LMLKHHDGAAH--KLVCYFTNWA-FSRPGSASILPRDLDPFLCTHLVFA 57

Qy         68 FAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYS 127
Db         58 FASMNNNQ--IVPKDPLD-------EKILYPEFNKLKERNRGLKTLLSVGGWNFGTSRFT 108

Qy        128 DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF 187
Db        109 KMLSTFSNRERFVKSVIALLRTHGFDGLDLFFLYPGLR-GSPARDRWTFVFLLEELLQAF 167

Qy        188 EPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
Db        168 KNEAQLTMRPRLLLSAAVSGDPHVIQKAYDARLLGRLLDFISVLSYDLHGSWEKVTGHNS 227

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
Db        228 PLFSLPGDPK------SSAYAMSYWRQLGVPPEKLLMGLPTYGRTFHLLRASQNELGAGA 281

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
Db        282 AGPASPGKYTKQAGFLAYYEVCSFVQRAKKRWINDQY--VPYAFKGKEWVGYDDAISFGY 339

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGH-CGP-KNPLLNKVHNMINGDEKNSFECILGPSTT 418
Db        340 KAFFIKREHFGGAMVWTLDLDDFRGNFCGTGPFPLAHTLNNLLVNDEFSS---------- 389

Qy        419 TPTP----TTTPTTPTTTPTTPSPTTPTTTPSPTTP--------TTTPSPTTPTTTPSPT 466
Db        390 TPSPKFWFSTAVNSSRIGPEMPTMTRDLTTGLGILPLGGEAVATETHRKSATMTTTPRGE 449

Qy        467 TPTPT-TP------TPAPTTSTPSPTTTEHTS 491
Db        450 TATPTRTPLSSGRRTAAPEGKTESPGEKPLTS 481
```

RESULT 9
I38605
oviductal glycoprotein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-May-1998
C;Accession: I38605
R;Arias, E.B.; Verhage, H.G.; Jaffe, R.C.
Biol. Reprod. 51, 685-694, 1994
A;Title: Complementary deoxyribonucleic acid cloning and molecular characterization of a
A;Reference number: I38605; MUID:95119256; PMID:7819450
A;Accession: I38605
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-654 <RES>
A;Cross-references: UNIPARC:UPI000017C2DA; EMBL:U09550; NID:g529147; PID:g529148

Query Match 21.5%; Score 668; DB 2; Length 654;
Best Local Similarity 33.1%; Pred. No. 8.4e-34;
Matches 176; Conservative 91; Mismatches 192; Indels 72; Gaps 19;

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Qy         10 IMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTI--EDIDPFKCTHLMYG 67
Db          4 LLLWVGLV---LVLKHHDGAAH--KLVCYFTNWA-HSRPGPASILPHDLDPFLCTHLIFA 57

Qy         68 FAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYS 127
Db         58 FASMNNNQI---VAKDLQD------EKILYPEFNKLKERNRELKTLLSIGGWNFGTSRFT 108

Qy        128 DMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF 187
Db        109 TMLSTFANREKFIASVISLLRTHDFDGLDLFFLYPGLR-GSPMHDRWTFLFLIEELLFAF 167

Qy        188 EPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
Db        168 RKEALLTMRPRLLLSAAVSGVPHIVQTSYDVRFLGRLLDFINVLSYDLHGSWERFTGHNS 227

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
Db        228 PLFSLPEDPK------SSAYAMNYWRKLGAPSEKLIMGIPTYGRTFRLLKASKNGLQARA 281

Qy        301 KGMSPPGFISGEEGVLSYIELCQLF--QKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASI 358
Db        282 IGPASPGKYTKQEGFLAYFEICSFVWGAKKHW----IDYQYVPYANKGKEWVGYDNAISF 337

Qy        359 SCKLAFLKELGVSGVMVWSLENDDFKG-HCGP-KNPLLNKVHNMINGDEKNSFECILGPS 416
Db        338 SYKAWFIRREHFGGAMVWTLDMDDVRGTFCGTGPFPLVYVLNDILVRAEFS--------S 389

Qy        417 TTTPT--PTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTP--------TTTPSPT 466
Db        390 TSLPQFWLSSAVNSSSTDPERLAVTTAWTTDSKILPPGGEAGVTEIHGKCENMTITPRGT 449

Qy        467 TPTPTTPT------------PAPTTSTPSPTTTEHTSETP--KYTTYVDGH 503
Db        450 TVTPTKETVSLGKHTVALGEKTEITGAMTMTSVGHQSMTPGEKALTPV-GH 499
```

RESULT 10
A49562
cartilage glycoprotein gp39 precursor - human
N;Alternate names: 39K synovial protein
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A49562; S10677; A33162
R;Hakala, B.E.; White, C.; Recklies, A.D.
J. Biol. Chem. 268, 25803-25810, 1993
A;Title: Human cartilage gp-39, a major secretory product of articular chondrocytes and
A;Reference number: A49562; MUID:94064658; PMID:8245017
A;Accession: A49562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-383 <HAK>
A;Cross-references: UNIPROT:P36222; UNIPARC:UPI0000126C19; GB:M80927; NID:g348911; PIDN:
R;Nyirkos, P.; Golds, E.E.
Biochem. J. 269, 265-268, 1990
A;Title: Human synovial cells secrete a 39 kDa protein similar to a bovine mammary pro
A;Reference number: S10677; MUID:90328983; PMID:2375755
A;Accession: S10677
A;Molecule type: protein
A;Residues: 22-40,'X',42-45 <NY2>
A;Cross-references: UNIPARC:UPI0000175A9E
C;Superfamily: Streptomyces chitinase chi40
C;Keywords: cartilage; extracellular protein; glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-383/Product: cartilage glycoprotein gp39 #status predicted <MAT>

Query Match 21.3%; Score 662; DB 2; Length 383;
Best Local Similarity 34.9%; Pred. No. 9.8e-34;
Matches 144; Conservative 81; Mismatches 136; Indels 52; Gaps 12;

```
Qy          2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIED-IDPFK 60
Db          7 QTGFVVLVLLQCC----------------SAYKLVCYYTSWSQYREGDGSCFPDALDRFL 50

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRG---YERFNNLRLKNPELTTMISLG 117
Db         51 CTHIIYSFANI-------------SNDHIDTWEWNDVTLYGMLNTLKNRNPNLKTLLSVG 97

Qy        118 GWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYL 177
Db         98 GWNFGSQRFSKIASNTQSRRTFIKSVPPFLRTHGFDGLDLAWLYPGRR------DKQHFT 151

Qy        178 ALVRELKDAF----EP--HGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGG 231
Db        152 TLIKEMKAEFIKEAQPGKKQLLLSAALSAGKVTIDSSYDIAKISQHLDFISIMTYDFHGA 211

Qy        232 WENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDR 291
Db        212 WRGTTGHHSPLF-RGQEDASPDRFSNTDYAVGYMLRLGAPASKLVMGIPTFGRSFTLAS- 269

Qy        292 SKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVG 351
Db        270 SETGVGAPISGPGIPGRFTKEAGTLAYYEICDFLRGATVHRTLGQ--QVPYATKGNQWVG 327

Qy        352 YDDLASISCKLAFLKELGVSGVMVWSLENDDFKG-HCGP--KNPLLNKVHNMI 401
Db        328 YDDQESVKSKVQYLKDRQLAGAMVWALDLDDFQGSFCGQDLRFPLTNAIKDAL 380
```

RESULT 11
S51327
heparin-binding glycoprotein 38K - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S51327
R;Shackelton, L.M.; Mann, D.M.; Millis, A.J.T.
submitted to the EMBL Data Library, January 1995
A;Description: Identification of a 38kDa heparin-binding glycoprotein (gp38k) in diffe
A;Reference number: S51327
A;Accession: S51327
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-383 <SHA>
A;Cross-references: UNIPROT:Q29411; UNIPARC:UPI0000088CC8; EMBL:Z47803; NID:g634097; P
C;Superfamily: Streptomyces chitinase chi40

Query Match 20.9%; Score 650; DB 2; Length 383;
Best Local Similarity 36.6%; Pred. No. 5.4e-33;
Matches 139; Conservative 77; Mismatches 130; Indels 34; Gaps 11;

```
Qy         34 RIVCYVGTWSVYHKVDPYTIED-IDPFKCTHLMYGFAKIDEYKY-TIQVFDPYQDDNHNS 91
Db         23 KLVCYYTSWSQYREGDGSCFPDAIDPFLCTHIIYSFANISNNEIDTLE------------ 70

Qy         92 W-EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEY 150
```

```
Db         71 WNDVTLYDTLNTLKNRNPNLKTLLSVGGWNFGSQRFSKIASNTQSRRTFIKSVPPFLRTH 130

Qy        151 KFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG------YLLTAAVSPGKDK 204
              |||||| |  || |      ||::   ||:|:|  |           ||: ||| ||
Db        131 GFDGLDLAWISPGRR------DKRHLTTLVKEMKAEFVREALPGTERLLLSGAVSAGKVA 184

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
              ||| ||| ::::  |:::::|||:|| |    ||::||::   :      : | :| : |
Db        185 IDRGYDIAQISQHLDFISLLTYDFHGAWRQTTGHHSPLFRGQGDASS-DRFSNADYAVSY 243

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
              |  ||  :|||||:| :||:::   ||  :| || |   ||  : |:|:|:| |:|
Db        244 VLRLGAPANKLVMGIPTFGRSFTLAS-SKTDVGAPASGPGIPGRFTKEKGILAYYEICDF 302

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
              |      ::       ||      ||||||  |:  |  :||   ::| |||:|: |||:
Db        303 LQGAT--VRRPLGQQVPYATKGNQWVGYDDQESVKNKAKYLKSRQLAGAMVWTLDLDDFR 360

Qy        385 GH-CGP--KNPLLNKVHNMI 401
              |: ||   : || : : :::
Db        361 GNFCGQNLRFPLTSAIKDVL 380


RESULT 12
S61551
breast-regressing protein brp39 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S61551; S61550; I48271
R;Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A;Title: neu and ras initiate murine mammary tumors that share genetic markers generally
A;Reference number: I48271; MUID:95060797; PMID:7970700
A;Accession: S61551
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-405 <MOR1>
A;Cross-references: UNIPROT:Q61362; UNIPARC:UPI0000175A9D; EMBL:X93035; NID:g1085065; PI
R;Morrison, B.W.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61550
A;Accession: S61550
A;Molecule type: mRNA
A;Residues: 1-245,'I',247-330,'H',332-350,'MVWALDLDDFQGTCQPKEFFPLTNAIKDALA' <MOR2>
A;Cross-references: UNIPARC:UPI000002841D; EMBL:X93035; NID:g1085065; PIDN:CAA63603.1; P
A;Note: the differences at the carboxyl end are due to a frameshift error
C;Genetics:
A;Gene: brp39
C;Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-405/Product: breast-regressing protein brp39 #status predicted <MAT>

  Query Match             20.8%;  Score 646.5;  DB 2;  Length 405;
  Best Local Similarity   34.4%;  Pred. No. 9.6e-33;
  Matches  140;  Conservative   73;  Mismatches  129;  Indels   65;  Gaps   12;

Qy         34 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
              ::|||  :|| | : |  :  : | || |||::| || |                |:  ::|
Db         23 KLVCYFTSWSQYREGVGSFLPDAIQPFLCTHIIYSFANIS-----------SDNMLSTW 70

Qy         93 E---KRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQE 149
              |   :  |:: | |: :|  | |::|:|||  | :::|::|:|   |  |::||  ||:
Db         71 EWNDESNYDKLNKLKTRNTNLKTLLSVGGWKFGEKRFSEIASNTERRTAFVRSVAPFLRS 130

Qy        150 YKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAF----EP--HGYLLTAAVSPGKD 203
              | |||||| | ||  |       ||| :  |::||   |    :|    ||:||:| ||
Db        131 YGFDGLDLAWLYPRLR------DKQYFSTLIKELNAEFTKEVQPGREKLLLSAALSAGKV 184

Qy        204 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH 263
              ||  ||| :: :  |::|:||||:|| |    ||::||::   :|      | |||| :
Db        185 AIDTGYDIAQIAQHLDFINLMTYDFHGVWRQITGHHSPLFQGQKDT-RFDRYSNVNYAVQ 243

Qy        264 YYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQ 323
              |    ||   ||:||:| :|:::::   |: :|| |  |   ||  : | | |:| |:|
Db        244 YMTRLGAQASKLLMGIPTFGKSFTLAS-SENQLGAPISGEGLPGRFTKEAGTLAYYEICD 302

Qy        324 LFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGV----MVWSLE 379
              :  | |   :|    |:      ||||:|  |:  |: ||||  ::|      :| :
Db        303 FLKGAEVHRLSNE--KVPFATKGNQWVGYEDKESVKNKVGFLKEKKLAGAWCGHWIWMI- 359

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTP 426
              |||  |||                          |: :|||:  |
Db        360 ----SGHCQPKN----------------------SSRSPTPSRMP 378


RESULT 13
S27879
secretory protein YM-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S27879
R;Chang, N.C.A.; Liu, C.H.; Chang, A.C.
submitted to the EMBL Data Library, June 1992
A;Description: Molecular characterization of a secretory protein (YM-1) transiently exp
A;Reference number: S27879
A;Accession: S27879
A;Molecule type: mRNA
A;Residues: 1-399 <CHA>
A;Cross-references: UNIPROT:O35744; UNIPARC:UPI0000175AA0; EMBL:M94584; NID:g202441; PI
C;Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-399/Product: secretory protein YM-1 #status predicted <MAT>

  Query Match             19.6%;  Score 608;  DB 2;  Length 399;
  Best Local Similarity   36.3%;  Pred. No. 2.3e-30;
  Matches  141;  Conservative   67;  Mismatches  140;  Indels   40;  Gaps   14;

Qy         34 RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKI--DEYKYTIQVFDPYQDDNHN 90
              :::||  :|:    ::  :   :|||  ||||:| || :  :|  ||           :
Db         23 QLMCYYTSWAKDRPIEGSFKPGNIDPCLCTHLIYAFAGMQNNEITYT-----------H 70

Qy         91 SWEKRGYERFNNLR-LKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQE 149
              : | ||  | |:  || || |:::|||  |    :| | : |  || |||||: ||::
Db         71 EQDLRDYEALNGLKDKKNTELKTLLAIGGWKFGPAPFSAMVSTPQNRQIFIQSVIRFLRQ 130

Qy        150 YKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGK 202
              | ||||:|||:||||| |:|  ||  :  ||:|:: |||            |||   | |
Db        131 YNFDGLNLDWQYPGSR-GSPPKDKHLFSVLVKEMRKAFEEESVEKDIPRLLLT---STGA 186

Qy        203 DKIDRAYD-IKELN--KLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
              ||       : ||   | |:: ||||| |   : : | |:|||| | :  :     ||:
Db        187 GIIDVIKSGTRSLNCLSLLDYIQVMTYDLHDPKDGYTGENSPLYKSPYDIGK-SADLNVD 245

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
              : |: ::||  :||::| | ||  : : | ||  :| |     |||  : | |:|:|
Db        246 SIISYWKDHGAASEKLIVGFPAYGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYY 305

Qy        320 ELCQLFQK---EEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVW 376
              |:|    :   | |    |     || |    |||||:: |   |  :||:  : | :||
Db        306 EVCTFLNEGATEVW----DAPQEVPYAYQGNEWVGYDNVRSFKLKAQWLKDNNLGGAVVW 361

Qy        377 SLENDDFKG-HCGPKN-PLLNKVHNMIN 402
              |: ||| |  |   :: || : :   :|
Db        362 PLDMDDFSGSFCHQRHFPLTSTLKGDLN 389


RESULT 14
A38221
chitinase (EC 3.2.1.14) MF1 - nematode (Brugia malayi)
C;Species: Brugia malayi
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A38221
R;Fuhrman, J.A.; Lane, W.S.; Smith, R.F.; Piessens, W.F.; Perler, F.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 1548-1552, 1992
A;Title: Transmission-blocking antibodies recognize microfilarial chitinase in brugian
A;Reference number: A38221; MUID:92179220; PMID:1542646
```

```
A;Accession: A38221
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-504 <FUH>
A;Cross-references: UNIPROT:P29030; UNIPARC:UPI0000127827; GB:M73689; NID:g156063; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIP:85345)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

  Query Match          19.5%;  Score 604.5;  DB 2;  Length 504;
  Best Local Similarity  30.1%;  Pred. No. 5e-30;
  Matches  156;  Conservative   86;  Mismatches  208;  Indels   69;  Gaps   17;

Qy         37 CYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQ-DDNHNSWEK 94
              ||    |: |   :  :   :|    |||::| |||:||    :    |:: :|    | |
Db         27 CYYTNWAQYRDGEGKFLPGNIPNGLCTHILYAFAKVDE----LGDSKPFEWNDEDTEWSK 82

Qy         95 RGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDG 154
                |      ||  || | ::| ||:  ||  :: :| :    ::||:| : ||::  |||
Db         83 GMYSAVTKLRETNPGLKVLLSYGGYNFGSAIFTGIAKSAQKTERFIKSAIAFLRKNNFDG 142

Qy        155 LDLDWEYP-GSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKE 213
               ||||||| |    : |: :    | | | | : :    ||||||| ||  || :|:::
Db        143 FDLDWEYPVGVAEEHAKLVEAMKTAFVEEAKTSGKQR-LLLTAAVSAGKGTIDGSYNVES 201

Qy        214 LNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRD 273
              | | || : :|:|| || ||     :  |:    |   :   ||  :   |: : |  ::
Db        202 LGKNFDLLFLMSYDLHGSWEKNVDLHGKLHPTKGEVSGI-GIFNTEFAADYWASKGMPKE 260

Qy        274 KLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQ 333
              |:::|:| | : |:::: |:  :|  |   |      :   |  || |:|: ::
Db        261 KIIIGIPMYAQGWTLDNPSETAIGAAASRPSSASKTNPAGGTASYWEICKYLKEGGKETV 320

Qy        334 YDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKG-HCGP-KN 391
              : |   | |       | |||:  :|  |: :||| |  |  :|:|: ||| |  ||
Db        321 HQEGVGA-YMVKGDQWYGYDNEETIRIKMKWLKEKGYGGAFIWALDFDDFTGKSCGKGPY 379

Qy        392 PLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTTPSPTTPT 451
              |||| : : : |: :|        |  ||  |: | |     |  |
Db        380 PLLNAISSELEGESEN-------PEITTEEPSITETEAYETDETEE-------------- 418

Qy        452 TTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY----VDGHLIKC 507
                          |: | |  |          || |||| : |||      :|   :|
Db        419 ------------------TSETEAYDTD-----ETEETSET-EATTYDTDETEGQ--EC 451

Qy        508 -YKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIW 545
               ::|  ||||: | :: |         ::| ||  | :
Db        452 PERDGLFPHPTDCHLFIQC----ANNIAYVMQCPATTFF 486


RESULT 15
D83764
chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83764
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-599 <STO>
A;Cross-references: UNIPROT:Q9KED7; UNIPARC:UPI00000C3A27; GB:AP001510; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0916

  Query Match          19.1%;  Score 592;  DB 2;  Length 599;
  Best Local Similarity  29.0%;  Pred. No. 3.7e-29;
  Matches  183;  Conservative   98;  Mismatches  216;  Indels  134;  Gaps   29;

Qy          2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKC 61
```

```
                | :  |::::  :  | |       : | :  :|| |  :|  | :   | : |||  |
Db          9 KLLIWIVTVLLVVTWMPADQVVGAAETSDDQYKIVAYYPSWGAYGR--DYQVWDIDASKI 66

Qy         62 THLMYGFAK---------------------------IDEYKYTIQVFDPYQD----DNH 89
               :|: | ||                          ||    :| : ||: |    :
Db         67 SHINYAFANICWDGRHGNPDPAGPNPQTWSCQDENGVIDVPNGSIVMGDPWIDAQKSNPG 126

Qy         90 NSWEK--RG-YERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDF 146
              ::|::  || ::: |.|: ::|  | |:||:|||    | ::|||||     |: |  | ::|
Db        127 DTWDEPLRGNFKQLNKLKEEHPHLKTLISVGGW-TWSNRFSDMAATKETRENFANSAVEF 185

Qy        147 LQEYKFDGLDLDWEYP--GSRLGNPK--IDKQNYLALVRELKDAFEPHG------YLLTA 196
              :::| |||:|:|||||  |   || :   ||:|:: |::|::|  :  |       ||||
Db        186 IRKYGFDGVDVDWEYPVSGGLPGNSRRPEDKENHVLLLQEVRDKLDEAGQEDGKDYLLTI 245

Qy        197 A--VSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETD-ELH 253
              |   |||  : ::   : |: :: ||:|:||||::|||:|  |||||||  |   : ||
Db        246 ASGASPGYVENNK---LNEIAEIVDWINIMTYDFNGGWQNISGHNAPLYYDPATANTELP 302

Qy        254 T--YFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISG 311
              |  :|||   :  :|  |   |||:|:||||| ||  | :    |:  :  :||   :
Db        303 TPEHFNVESAVEGHLQAGVPEHKLVLGMPFYGRGWSNCDGA--NQGEYQR-CAPPREGTW 359

Qy        312 EEGVLSYIELCQLFQKEEWHIQ---YDEYYN----APYGYN--DKIWVGYDDLASISCKL 362
              | ||  : :|       |: :|    |  |:|      |: ||  :  :: |||  |   |
Db        360 ENGVFDFSDL------EDHYINKNGYQRYWNDVAKVPFLYNATNGNFITYDDEESFRYKT 413

Qy        363 AFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTP 422
              |:|   ::| | | : |                    ||    :   ||    ||
Db        414 DFIKSNNLAGSMFWDVSGDR------------------NGTLLTALADQLG---FTPHE 451

Qy        423 TTTPTTPTTTPTTPSPTTPTTTPSPTT---PTTTPSPTTPTTTPSPTTPTPTTPT---PA 476
                |  |:: ||   |  |:|    |   ||  |:  :          | | || |
Db        452 GQEPEEPSSAPTNIQATEVTSTTVTLTWQAPTEEPTQYSVAYDSKEKTTTHTTITIEDLQ 511

Qy        477 PTTSTPSPTTTEH----------TSETPKYTTYVDG------HLIKCYKEGD-IPHPTNI 519
              | |:     : ||           | |  |  ||           |  || : |   :
Db        512 PETTYTFVVSAEHKDGIRHAGQALQVTTKSETGGDGCTAPTWQANNVYTGGDQVQHGGKL 571

Qy        520 HKYLVCEFVNGGWWVHIMPCPPGT-----IW 545
              ::           ||       |||     :|
Db        572 YE--------AKWWT--TGEEPGTTGEWGVW 592


Search completed: March 31, 2006, 15:08:47
Job time : 43 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:42:20 ; Search time 167 Seconds
(without alignments)
1388.594 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 35

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	555	100.0	555	4	US-10-218-743-15	Sequence 15, Appl
2	555	100.0	555	4	US-10-218-743-18	Sequence 18, Appl
3	536	96.6	536	4	US-10-218-743-21	Sequence 21, Appl
4	64	11.5	490	4	US-10-218-743-41	Sequence 41, Appl
5	64	11.5	509	4	US-10-218-743-35	Sequence 35, Appl
6	64	11.5	509	4	US-10-218-743-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match 100.0%; Score 555; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
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Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
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Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
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Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
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RESULT 2
US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13

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;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-18

  Query Match             100.0%;  Score 555;  DB 4;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
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Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
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Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
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Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
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Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
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Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
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Db        541 PGTIWCQEKLTCIGE 555


RESULT 3
US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 536
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-21

  Query Match             96.6%;  Score 536;  DB 4;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
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Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
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Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
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Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555
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Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536


RESULT 4
US-10-218-743-41
; Sequence 41, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
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;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 490
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-41

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  Best Local Similarity   100.0%;  Pred. No. 1.5e-54;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        292 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 351

Qy        371 SGVM 374
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Db        352 SGVM 355


RESULT 5
US-10-218-743-35
; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 509
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-35

  Query Match             11.5%;  Score 64;  DB 4;  Length 509;
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  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        371 SGVM 374
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Db        371 SGVM 374


RESULT 6
US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 509
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-38

  Query Match             11.5%;  Score 64;  DB 4;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-54;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
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Qy        371 SGVM 374
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Db        371 SGVM 374


Search completed: March 31, 2006, 15:46:00
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GenCore version 5.1.7

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Run on: March 31, 2006, 15:08:21 ; Search time 48 Seconds
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Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3107	100.0	555	2	US-09-292-225-18	Sequence 18, Appl
3	3014	97.0	536	2	US-09-292-225-21	Sequence 21, Appl
4	2542	81.8	509	2	US-09-292-225-35	Sequence 35, Appl
5	2542	81.8	509	2	US-09-292-225-38	Sequence 38, Appl
6	2475	79.7	490	2	US-09-292-225-41	Sequence 41, Appl
7	838.5	27.0	554	1	US-08-524-051-2	Sequence 2, Appli
8	838.5	27.0	554	2	US-09-052-778-16	Sequence 16, Appl
9	815.5	26.2	583	2	US-09-545-814-2	Sequence 2, Appli
10	815.5	26.2	583	2	US-09-545-814-5	Sequence 5, Appli
11	812.5	26.2	635	2	US-09-545-814-32	Sequence 32, Appl
12	811.5	26.1	559	2	US-09-545-814-14	Sequence 14, Appl
13	738	23.8	466	1	US-08-486-839-4	Sequence 4, Appli
14	738	23.8	466	2	US-09-151-011-4	Sequence 4, Appli
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16	738	23.8	466	2	US-09-343-623-4	Sequence 4, Appli
17	738	23.8	466	2	US-08-877-599-2	Sequence 2, Appli
18	738	23.8	466	2	US-09-267-574-2	Sequence 2, Appli
19	738	23.8	466	2	US-09-977-827-4	Sequence 4, Appli
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24	732.5	23.6	387	2	US-09-977-827-6	Sequence 6, Appli
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29	721.5	23.2	373	2	US-09-039-198A-15	Sequence 15, Appl
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32	721.5	23.2	373	2	US-09-267-574-14	Sequence 14, Appl
33	721.5	23.2	373	2	US-09-267-574-15	Sequence 15, Appl
34	708.5	22.8	455	2	US-10-130-158A-1	Sequence 1, Appli
35	708.5	22.8	476	2	US-10-130-158A-5	Sequence 5, Appli
36	708.5	22.8	476	2	US-10-268-919-5	Sequence 5, Appli
37	672.5	21.6	489	2	US-09-545-814-29	Sequence 29, Appl
38	669	21.5	682	2	US-09-949-016-10624	Sequence 10624, A
39	662	21.3	383	2	US-09-949-016-6053	Sequence 6053, Ap
40	658	21.2	365	2	US-09-949-016-7947	Sequence 7947, Ap
41	650	20.9	383	2	US-09-459-749D-17	Sequence 17, Appl
42	640.5	20.6	377	2	US-10-130-158A-18	Sequence 18, Appl
43	640.5	20.6	398	2	US-10-130-158A-17	Sequence 17, Appl
44	632	20.3	396	2	US-09-949-016-8736	Sequence 8736, Ap
45	630	20.3	385	1	US-08-694-915-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-292-225-15
; Sequence 15, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match 100.0%; Score 3107; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
                |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555


RESULT 2
US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT: Hunter, Shirley Wu
;  APPLICANT: Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/09/292,225
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: 60/098,909
;  EARLIER FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/085,295
;  EARLIER FILING DATE: 1998-05-13
;  EARLIER APPLICATION NUMBER: 60/098,565
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: 09/062,013
;  EARLIER FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-09-292-225-18

  Query Match             100.0%;  Score 3107;  DB 2;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-239;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
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Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
                |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555


RESULT 3
US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT: Hunter, Shirley Wu
;  APPLICANT: Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/09/292,225
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: 60/098,909
;  EARLIER FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/085,295
;  EARLIER FILING DATE: 1998-05-13
;  EARLIER APPLICATION NUMBER: 60/098,565
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: 09/062,013
;  EARLIER FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 536
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-09-292-225-21

  Query Match             97.0%;  Score 3014;  DB 2;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 3e-232;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79
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Db          1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 60

Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240
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Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
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Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 420

Qy        440 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 480

Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536
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RESULT 4
US-09-292-225-35
; Sequence 35, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-35

Query Match 81.8%; Score 2542; DB 2; Length 509;
Best Local Similarity 81.7%; Pred. No. 1.3e-194;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

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Db          1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              |||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQPIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| ||
Db        121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||:|||| |||||||||||||||| ||::||||:|||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              |||||||||||||:||||||||||||||| ||||||||||||||||:||:|||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||  || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                 ||||: ||||||||||:|||||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
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Db        492 DCPKGTRWHATLKNCIQE 509
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RESULT 5
US-09-292-225-38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

Query Match 81.8%; Score 2542; DB 2; Length 509;
Best Local Similarity 81.7%; Pred. No. 1.3e-194;
Matches 456; Conservative 24; Mismatches 26; Indels 52; Gaps 2;

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Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
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Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| ||
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Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||:|||| |||||||||||||||| ||::||||:|||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

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              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              |||||||||||||:|||||||||||||||| ||||||||||||||:||:||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||  || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                  ||||: |||||||||||:|||||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
               || || |      || |
Db        492 DCPKGTRWHATLKNCIQE 509


RESULT 6
US-09-292-225-41
; Sequence 41, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT: Hunter, Shirley Wu
;  APPLICANT: Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/09/292,225
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: 60/098,909
;  EARLIER FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/085,295
;  EARLIER FILING DATE: 1998-05-13
;  EARLIER APPLICATION NUMBER: 60/098,565
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: 09/062,013
;  EARLIER FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 490
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-09-292-225-41

  Query Match             79.7%;  Score 2475;  DB 2;  Length 490;
  Best Local Similarity   82.5%;  Pred. No. 2.8e-189;
  Matches  443;  Conservative   21;  Mismatches   21;  Indels   52;  Gaps    2;

Qy         22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 81
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 62

Qy         82 DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
              ||:|||||||||| |||||||||||||||||||||||||||||||||||||||||||:|
Db         63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122

Qy        142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
              |||||||||||||||||||||||||||||||||| ||||||:|||| ||||||||||
Db        123 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG 182

Qy        202 KDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
              ||||| ||::||||:|||||||||||||||| :|||||||||||||||||||||||||
Db        183 KDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 242

Qy        262 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 321
              |||||||||||||||||||||||||||||:|||||||||||||:||||||||||
Db        243 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 302

Qy        322 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 381
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        303 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362

Qy        382 DFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTTPTTPSPTTP 441
              ||||||||| |||||||||||||||:||:|||||||||||   || |||||
Db        363 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTPTTPSTTSTTTPT------- 415

Qy        442 TTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVD 501
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Db        416 ----------------------------------------PTTTDSTSETPKYTTYID 433

Qy        502 GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 555
              ||||||||:| :||||::||||||::   |||||||||| || || |      || |
Db        434 GHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIMDCPKGTRWHATLKNCIQE 490


RESULT 7
US-08-524-051-2
; Sequence 2, Application US/08524051
; Patent No. 5866788
;  GENERAL INFORMATION:
;    APPLICANT:  Kramer, Karl J.
;    APPLICANT:  Muthukrishnan, Subbaratnam
;    APPLICANT:  Choi, Hee Kyung
;    APPLICANT:  Corpuz, Lolita
;    APPLICANT:  Gopalakrishnan, Bhuvana
;    TITLE OF INVENTION:  RECOMBINANT CHITINASE AND USE THEREOF AS
;    TITLE OF INVENTION:  A BIOCIDE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hovey, Williams, Timmons & Collins
;      STREET:  2405 Grand Blvd., Suite 400
;      CITY:  Kansas City
;      STATE:  MO
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/524,051
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Collins, John M.
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  22875-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (816)474-9050
;      TELEFAX:  (816)474-9057
;      TELEX:  434-363
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  554 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-524-051-2

  Query Match             27.0%;  Score 838.5;  DB 1;  Length 554;
  Best Local Similarity   35.4%;  Pred. No. 1.4e-58;
  Matches  208;  Conservative   79;  Mismatches  210;  Indels   91;  Gaps   20;

Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
              | |: :| : |  |         | :  |||||   |:||   |  | ||||   ||||:
Db          3 ATLATLAVLALATAV-------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI 55
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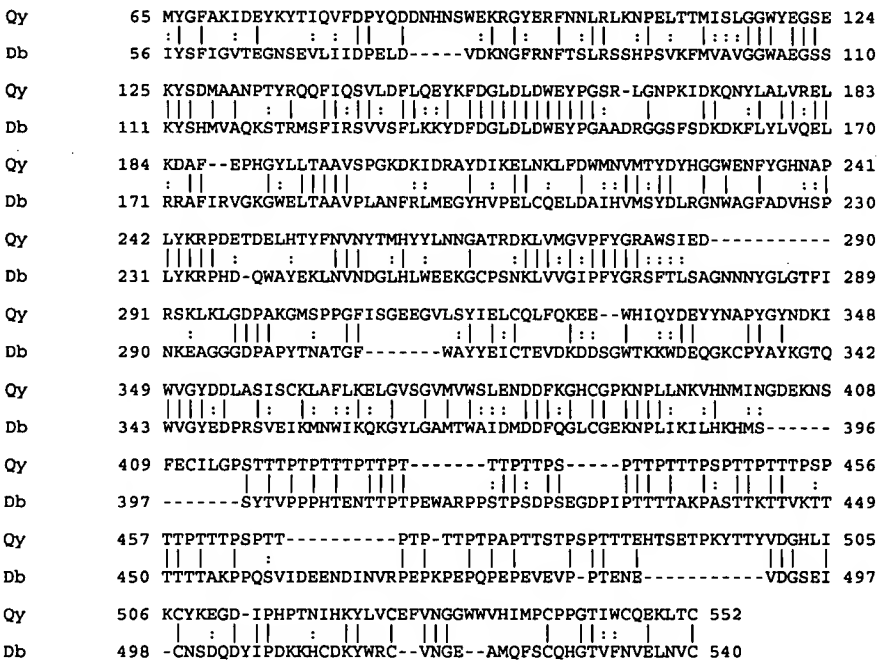
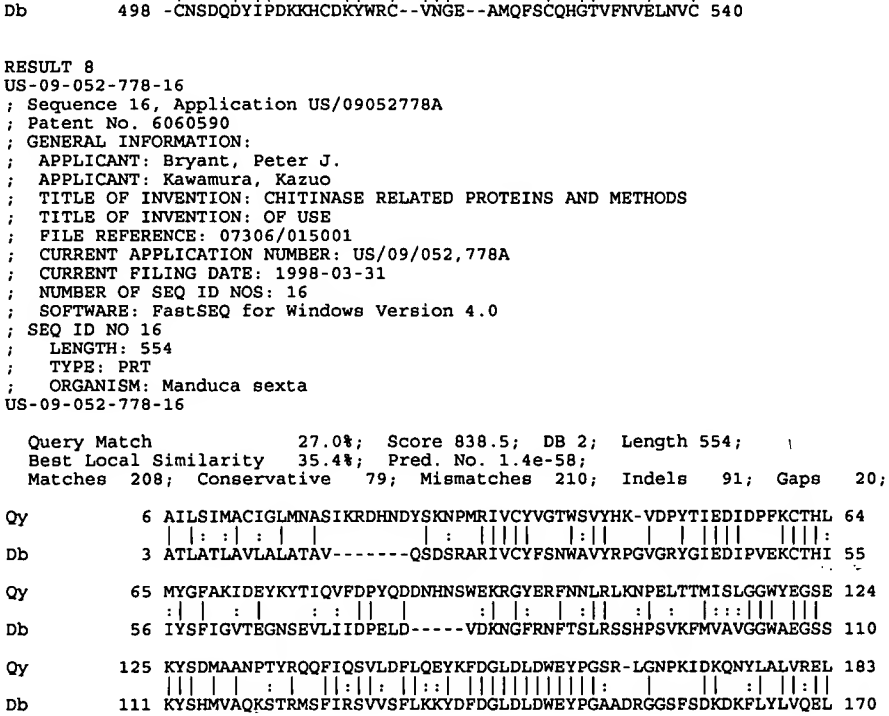


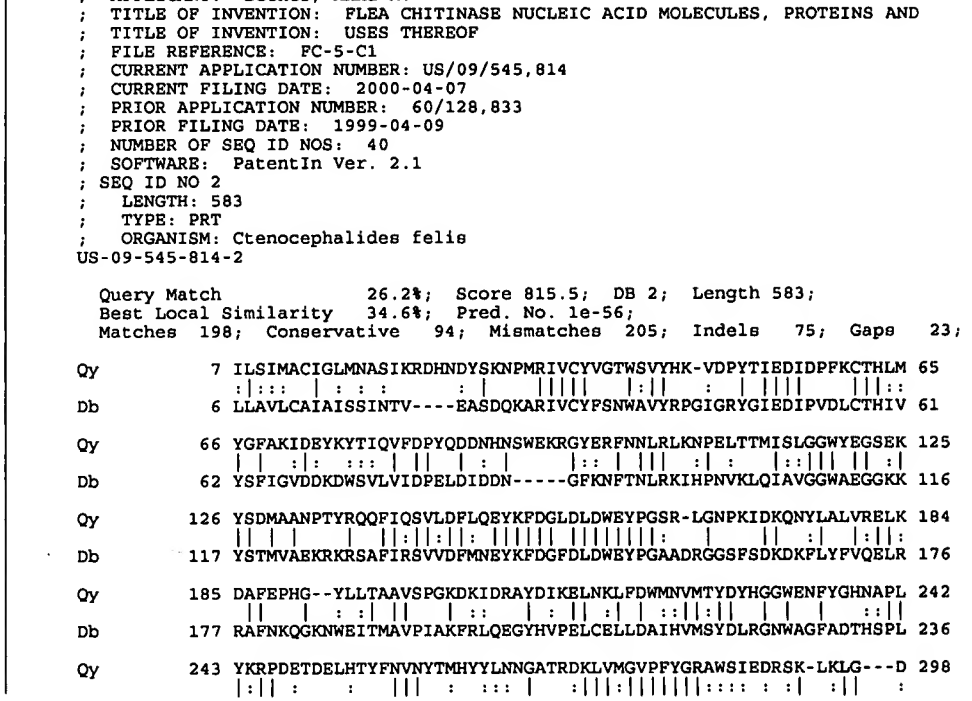
RESULT 8
US-09-052-778-16
; Sequence 16, Application US/09052778A
; Patent No. 6060590
; GENERAL INFORMATION:
; APPLICANT: Bryant, Peter J.
; APPLICANT: Kawamura, Kazuo
; TITLE OF INVENTION: CHITINASE RELATED PROTEINS AND METHODS
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 07306/015001
; CURRENT APPLICATION NUMBER: US/09/052,778A
; CURRENT FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-052-778-16

Query Match 27.0%; Score 838.5; DB 2; Length 554;
Best Local Similarity 35.4%; Pred. No. 1.4e-58;
Matches 208; Conservative 79; Mismatches 210; Indels 91; Gaps 20;



RESULT 9
US-09-545-814-2
; Sequence 2, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
; APPLICANT: Becher, Anna M.
; TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: FC-5-C1
; CURRENT APPLICATION NUMBER: US/09/545,814
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,833
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Ctenocephalides felis
US-09-545-814-2

Query Match 26.2%; Score 815.5; DB 2; Length 583;
Best Local Similarity 34.6%; Pred. No. 1e-56;
Matches 198; Conservative 94; Mismatches 205; Indels 75; Gaps 23;



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Db        237 YRRPHD-QYAYEKLNVNDGLQLWVDMGCPANKLVVGVPFYGRSFTLSNSNKDYRLGTYIN 295

Qy        299 PAKGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLA 356

Db        296 KEAGGGEPGPYTNATGFISYYEICLEVDDPSKGWTKKWDEHGKVPYAYKGNQWVGYEDPK 355

Qy        357 SISCKLAFLKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGP 415

Db        356 SVALKMEFIKSKGYGGAMTWAIDMDDFQGVCSDDKHTLAVIMHDYM----KNYIVPEFDS 411

Qy        416 STTTPTP--TTTPTTPTTTPTTPSPTTPTT-TPSPT-TPTTTPSPTTPTTTPSPTTPTPT 471

Db        412 SRITPRPEWAKPPSTPSQEP-DDTPYIPTTHAPKPSRKPTRKPKPT--TTTVAATTPVAT 468

Qy        472 TPTPAPTTSTPSPTTTE-----HTSETP---------KYTTYVDGHLIKCYKEGDIPHPT 517

Db        469 ------------TTTEHHHHHHEEEKPSEQDNQVGSQDTTATD---VDCSQEDYLPH-E 511

Qy        518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545

Db        512 DCNKYYRC--------VHGEAVLFTCREGTVY 535


RESULT 10
US-09-545-814-5
; Sequence 5, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
;  APPLICANT:  Becher, Anna M.
;  TITLE OF INVENTION:  FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  FC-5-C1
;  CURRENT APPLICATION NUMBER: US/09/545,814
;  CURRENT FILING DATE:  2000-04-07
;  PRIOR APPLICATION NUMBER:  60/128,833
;  PRIOR FILING DATE:  1999-04-09
;  NUMBER OF SEQ ID NOS:  40
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 583
;   TYPE: PRT
;   ORGANISM: Ctenocephalides felis
US-09-545-814-5

  Query Match             26.2%;  Score 815.5;  DB 2;  Length 583;
  Best Local Similarity   34.6%;  Pred. No. 1e-56;
  Matches  198;  Conservative   94;  Mismatches  205;  Indels   75;  Gaps   23;

Qy          7 ILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLM 65

Db          6 LLAVLCAIAISSINTV----EASDQKARIVCYFSNWAVYRPGIGRYGIEDIPVDLCTHIV 61

Qy         66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125

Db         62 YSFIGVDDKDWSVLVIDPELDIDDN-----GFKNFTNLRKIHPNVKLQIAVGGWAEGGKK 116

Qy        126 YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVRELK 184

Db        117 YSTMVAEKRKRSAFIRSVVDFMNEYKFDGFDLDWEYPGAADRGGSFSDKDKFLYFVQELR 176

Qy        185 DAFEPHG--YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPL 242

Db        177 RAFNKQGKNWEITMAVPIAKFRLQEGYHVPELCELLDAIHVMSYDLRGNWAGFADTHSPL 236

Qy        243 YKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSK-LKLG---D 298

Db        237 YRRPHD-QYAYEKLNVNDGLQLWVDMGCPANKLVVGVPFYGRSFTLSNSNKDYRLGTYIN 295

Qy        299 PAKGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLA 356

Db        296 KEAGGGEPGPYTNATGFISYYEICLEVDDPSKGWTKKWDEHGKVPYAYKGNQWVGYEDPK 355

Qy        357 SISCKLAFLKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGP 415

Db        356 SVALKMEFIKSKGYGGAMTWAIDMDDFQGVCSDDKHTLAVIMHDYM----KNYIVPEFDS 411

Qy        416 STTTPTP--TTTPTTPTTTPTTPSPTTPTT-TPSPT-TPTTTPSPTTPTTTPSPTTPTPT 471

Db        412 SRITPRPEWAKPPSTPSQEP-DDTPYIPTTHAPKPSRKPTRKPKPT--TTTVAATTPVAT 468

Qy        472 TPTPAPTTSTPSPTTTE-----HTSETP---------KYTTYVDGHLIKCYKEGDIPHPT 517

Db        469 ------------TTTEHHHHHHEEEKPSEQDNQVGSQDTTATD---VDCSQEDYLPH-E 511

Qy        518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545

Db        512 DCNKYYRC--------VHGEAVLFTCREGTVY 535


RESULT 11
US-09-545-814-32
; Sequence 32, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
;  APPLICANT:  Becher, Anna M.
;  TITLE OF INVENTION:  FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  FC-5-C1
;  CURRENT APPLICATION NUMBER: US/09/545,814
;  CURRENT FILING DATE:  2000-04-07
;  PRIOR APPLICATION NUMBER:  60/128,833
;  PRIOR FILING DATE:  1999-04-09
;  NUMBER OF SEQ ID NOS:  40
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 635
;   TYPE: PRT
;   ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-32

  Query Match             26.2%;  Score 812.5;  DB 2;  Length 635;
  Best Local Similarity   34.6%;  Pred. No. 2e-56;
  Matches  198;  Conservative   93;  Mismatches  206;  Indels   75;  Gaps   23;

Qy          7 ILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLM 65

Db          7 LLAVLCAIAISSINTV----EASDQKARIVCYFSNWAVYRPGIGRYGIEDIPVDLCTHIV 62

Qy         66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125

Db         63 YSFIGVDDKDWSVLVIDPELDIDDN-----GFKNFTNLRKIHPNVKLQIAVGGWAEGGKK 117

Qy        126 YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVRELK 184

Db        118 YSTMVAEKRKRSAFIRSVVDFMNEYKFDGFDLDWEYPGAADRGGSFSDKDKFLYFVQELR 177

Qy        185 DAFEPHG--YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPL 242

Db        178 RAFNKQGKNWEITMAVPIAKFRLQEGYHVPELCELLDAIHVMSYDLRGNWAGFADTHSPL 237

Qy        243 YKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSK-LKLG---D 298

Db        238 YRRPHD-QYAYEKLNVNDGLQLWVDMGCPANKLVVGVPFYGRFFTLSNSNKDYRLGTYIN 296

Qy        299 PAKGMSPPGFISGEEGVLSYIELCQLFQ--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLA 356

Db        297 KEAGGGEPGPYTNATGFISYYEICLEVDDPSKGWTKKWDEHGKVPYAYKGNQWVGYEDPK 356

Qy        357 SISCKLAFLKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGP 415

Db        357 SVALKMEFIKSKGYGGAMTWAIDMDDFQGVCSDDKHTLAVIMHDYM----KNYIVPEFDS 412

Qy        416 STTTPTP--TTTPTTPTTTPTTPSPTTPTT-TPSPT-TPTTTPSPTTPTTTPSPTTPTPT 471

Db        413 SRITPRPEWAKPPSTPSQEP-DDTPYIPTTHAPKPSRKPTRKPKPT--TTTVAATTPVAT 469
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Qy        472 TPTPAPTTSTPSPTTTE-----HTSETP---------KYTTYVDGHLIKCYKEGDIPHPT 517
Db        470 ------------TTTEHHHHHHEEEKPSEQDNQVGSQDTTATD---VDCSQEDYLPH-E 512

Qy        518 NIHKYLVCEFVNGGWWVH----IMPCPPGTIW 545
Db        513 DCNKYYRC--------VHGEAVLFTCREGTVY 536


RESULT 12
US-09-545-814-14
; Sequence 14, Application US/09545814
; Patent No. 6416977
; GENERAL INFORMATION:
;  APPLICANT:  Becher, Anna M.
;  TITLE OF INVENTION:  FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  FC-5-C1
;  CURRENT APPLICATION NUMBER: US/09/545,814
;  CURRENT FILING DATE:  2000-04-07
;  PRIOR APPLICATION NUMBER:  60/128,833
;  PRIOR FILING DATE:  1999-04-09
;  NUMBER OF SEQ ID NOS:  40
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Ctenocephalides felis
US-09-545-814-14

  Query Match             26.1%;  Score 811.5;  DB 2;  Length 559;
  Best Local Similarity   35.8%;  Pred. No. 2e-56;
  Matches  195;  Conservative   86;  Mismatches  193;  Indels   71;  Gaps   22;

Qy         34 RIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
Db          5 RIVCYFSNWAVYRPGIGRYGIEDIPVDLCTHIVYSFIGVDDKDWSVLVIDPELDIDDN-- 62

Qy         93 EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKF 152
Db         63 ---GFKNFTNLRKIHPNVKLQIAVGGWAEGGKKYSTMVAEKRKRSAFIRSVVDFMNEYKF 119

Qy        153 DGLDLDWEYPGSR-LGNPKIDKQNYLALVRELKDAFEPHG--YLLTAAVSPGKDKIDRAY 209
Db        120 DGFDLDWEYPGAADRGGSFSDKDKFLYFVQELRRAFNKQGKNWEITMAVPIAKFRLQEGY 179

Qy        210 DIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNG 269
Db        180 HVPELCELLDAIHVMSYDLRGNWAGFADTHSPLYRRPHD-QYAYEKLNVNDGLQLWVDMG 238

Qy        270 ATRDKLVMGVPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGVLSYIELCQLF 325
Db        239 CPANKLVVGVPFYGRSFTLSNSNKDYRLGTYINKEAGGGEPGPYTNATGFISYYEICLEV 298

Qy        326 Q--KEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDF 383
Db        299 DDPSKGWTKKWDEHGKVPYAYKGNQWVGYEDPKSVALKMEFIKSKGYGGAMTWAIDMDDF 358

Qy        384 KGHCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPTP--TTTPTTPTTTPTTPSPTT 440
Db        359 QGVCSDDKHTLAVIMHDYM----KNYIVPEFDSSRITPRPEWAKPPSTPSQEP-DDTPYI 413

Qy        441 PTT-TPSPT-TPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTE-----HTSET 493
Db        414 PTTHAPKPSRKPTRKPKPT--TTTVAATTPVAT------------TTTEHHHHHHEEEK 458

Qy        494 P---------KYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVH----IMPCP 540
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Qy        541 PGTIW 545
Db        507 EGTVY 511


RESULT 13
US-08-486-839-4
; Sequence 4, Application US/08486839
; Patent No. 5928928
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  A human chitinase, its recombinant
;    TITLE OF INVENTION:  production, its use for decomposing chitin, its use
;    TITLE OF INVENTION:  in therapy or prophylaxis against infection diseases.
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann & Baron
;      STREET:  350 Jericho Turnpike
;      CITY:  Jericho
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  11758
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,839
;      FILING DATE:  07 - June - 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baron, Ronald J.
;      REGISTRATION NUMBER:  29,281
;      REFERENCE/DOCKET NUMBER:  294-26
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 822-3550
;      TELEFAX:  (516) 822-3582
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-08-486-839-4

  Query Match             23.8%;  Score 738;  DB 1;  Length 466;
  Best Local Similarity   34.2%;  Pred. No. 1.2e-50;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
Db         23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 71

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
Db         72 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 131

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
Db        132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 190

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
Db        191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
Db        250 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 309

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
Db        310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366
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Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
Db        367 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 394

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
Db        395 PELEVP-KPGQPSEPEHGPSPGQDT 418


RESULT 14
US-09-151-011-4
; Sequence 4, Application US/09151011
; Patent No. 6057142
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  A Human Chitinase, Its Recombinant
;    TITLE OF INVENTION:  Production, Its Use For Decomposing Chitin, Its Use in
;    TITLE OF INVENTION:  Therapy or Prophylaxis Against Infection Diseases.
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann & Baron, LLP
;      STREET:  6900 Jericho Turnpike
;      CITY:  Syosset
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  11791
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/151,011
;      FILING DATE:  10 - September - 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Morriss, Robert C.
;      REGISTRATION NUMBER:  42,910
;      REFERENCE/DOCKET NUMBER:  294-32 DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 822-3550
;      TELEFAX:  (516) 822-3582
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-09-151-011-4

  Query Match             23.8%;  Score 738;  DB 2;  Length 466;
  Best Local Similarity   34.2%;  Pred. No. 1.2e-50;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
Db         23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 71

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
Db         72 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 131

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
Db        132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 190

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
Db        191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGPISGEEGVLSYIELCQL 324
Db        250 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 309

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
Db        310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
Db        367 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 394

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
Db        395 PELEVP-KPGQPSEPEHGPSPGQDT 418


RESULT 15
US-09-039-198A-2
; Sequence 2, Application US/09039198A
; Patent No. 6200951
;  GENERAL INFORMATION:
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Tjoelker, Larry W.
;    TITLE OF INVENTION:  CHITINASE CHITIN-BINDING FRAGMENTS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/039,198A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  27866/34391
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-039-198A-2

  Query Match             23.8%;  Score 738;  DB 2;  Length 466;
  Best Local Similarity   34.2%;  Pred. No. 1.2e-50;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
Db         23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 71

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
Db         72 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 131

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
Db        132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 190

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
```

```
                :|  |:: :: :  |::|:| ||:|| ||   |||:||||| :|:    :  ||:  :
Db        191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
                :|  |    ||::|:| |||::::   |  ::| || |   ||  : | |:|:| |:|
Db        250 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 309

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                  :  || |:    || : |  |||:||: |   |:::||: |: | |||:|: |||
Db        310 KGATKQRIQ-DQ--KVPYIFRDNQWVGPDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSPECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
                |                      | |  |          |   |       |  |: |
Db        367 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 394

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
                |    |     |: |   |||   |
Db        395 PELEVP-KPGQPSEPEHGPSPGQDT 418
```

Search completed: March 31, 2006, 15:09:40
Job time : 50 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:00:56 ; Search time 235 Seconds
(without alignments)
1666.248 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3107	100.0	555	2	Q9U6R7_DERFA	Q9u6r7 dermatophag
2	2816.5	90.7	558	2	Q4JK70_DERPT	Q4jk70 dermatophag
3	2744.5	88.3	532	2	Q4JK69_DERPT	Q4jk69 dermatophag
4	1008.5	32.5	525	2	O44079_ANOGA	O44079 anopheles g
5	1006.5	32.4	525	2	Q7Q5I7_ANOGA	Q7q5i7 anopheles g
6	942	30.3	431	2	Q8ISH5_9ARAC	Q8ish5 araneus ven
7	869	28.0	1635	2	O17412_AEDAE	O17412 aedes aegyp
8	863	27.8	493	2	Q56JI1_9HYME	Q56ji1 toxoneuron
9	854.5	27.5	4498	2	Q9W2Z3_DROME	Q9w2z3 drosophila
10	851	27.4	2083	2	Q7PWC2_ANOGA	Q7pwc2 anopheles g
11	847	27.3	544	2	Q9GQC4_BOMMO	Q9gqc4 bombyx mori
12	842	27.1	476	2	Q9W2M7_DROME	Q9w2m7 drosophila
13	842	27.1	2838	2	Q8MP05_TENMO	Q8mp05 tenebrio mo
14	839	27.0	566	2	Q8WR52_BOMMO	Q8wr52 bombyx mori
15	838.5	27.0	554	1	CHIT_MANSE	P36362 manduca sex
16	837.5	27.0	467	2	O15993_PENJP	O15993 penaeus jap
17	837.5	27.0	543	2	Q9GR93_BOMMO	Q9gr93 bombyx mori
18	837.5	27.0	543	2	Q9GV05_BOMMO	Q9gv05 bombyx mori
19	837.5	27.0	565	2	P90710_BOMMO	P90710 bombyx mori
20	837.5	27.0	595	2	Q9VFR3_DROME	Q9vfr3 drosophila
21	831.5	26.8	467	2	Q8ITU3_PENVA	Q8itu3 penaeus van
22	829.5	26.7	565	2	Q9GPG9_BOMMA	Q9gpg9 bombyx mand
23	829.5	26.7	588	2	Q6VUB9_HELAM	Q6vub9 helicoverpa
24	823.5	26.5	557	2	Q8MTK0_CHOFU	Q8mtk0 choristoneu
25	823	26.5	488	2	Q90W34_BUFJA	Q90w34 bufo japoni
26	819.5	26.4	533	2	Q5QE61_TRICA	Q5qe61 tribolium c
27	814.5	26.2	552	2	Q9GV44_SPOLT	Q9gv44 spodoptera
28	810	26.1	574	2	O17411_AEDAE	O17411 aedes aegyp
29	808	26.0	552	2	Q6EHZ5_SPOLT	Q6ehz5 spodoptera
30	802	25.8	483	2	Q23737_9HYME	Q23737 chelonus sp
31	800.5	25.8	555	2	Q6QSW1_SPOFR	Q6qsw1 spodoptera
32	799	25.7	471	2	Q6NZZ8_BRARE	Q6nzz8 brachydanio
33	798	25.7	572	2	Q26042_PENJP	Q26042 penaeus jap
34	796	25.6	566	2	Q7PQX4_ANOGA	Q7pqx4 anopheles g
35	795	25.6	2286	2	Q7PL80_DROME	Q7pl80 drosophila
36	793.5	25.5	489	2	Q6GP67_XENLA	Q6gp67 xenopus lae
37	790.5	25.4	553	2	Q704Y2_9NEOP	Q704y2 lacanobia o
38	790	25.4	620	2	Q9Y0D4_PENMO	Q9y0d4 penaeus mon
39	787	25.3	553	2	P91731_HYPCU	P91731 hyphantria
40	780	25.1	470	2	Q803B7_BRARE	Q803b7 brachydanio
41	780	25.1	470	2	Q6P006_BRARE	Q6p006 brachydanio
42	776.5	25.0	456	2	Q7Q6W6_ANOGA	Q7q6w6 anopheles g
43	772	24.8	492	2	Q6DJ52_XENTR	Q6dj52 xenopus tro
44	770	24.8	484	2	Q75WB9_PAROL	Q75wb9 paralichthy
45	768.5	24.7	470	2	Q4L129_9DIPT	Q4l129 phlebotomus

ALIGNMENTS

RESULT 1
Q9U6R7_DERFA
ID Q9U6R7_DERFA PRELIMINARY; PRT; 555 AA.
AC Q9U6R7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 98kDa HDM allergen.
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21189488; PubMed=11292526; DOI=10.1016/S0165-2427(00)00258-0;
RA McCall C., Hunter S., Stedman K., Weber E., Hillier A., Bozic C.,
RA Rivoire B., Olivry T.;
RT "Characterization and cloning of a major high molecular weight house
RT dust mite allergen (Der f 15) for dogs.";
RL Vet. Immunol. Immunopathol. 78:231-247(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Weber E.R., Hunter S., Stedman K., McCall C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF178772; AAD52672.1; -; mRNA.
DR HSSP; Q13231; 1LG2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase_II.
DR InterPro; IPR002557; Chitin_bind_PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 555 AA; 63238 MW; 0E4564A1A459B30B CRC64;

Query Match 100.0%; Score 3107; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.5e-166;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
```

```
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555

Db        541 PGTIWCQEKLTCIGE 555
```

RESULT 2
Q4JK70_DERPT
ID Q4JK70_DERPT PRELIMINARY; PRT; 558 AA.
AC Q4JK70;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Group 15 allergen protein.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT "Der p 15-A chitinase allergen from Dermatophagoides pteronyssinus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; DQ078740; AAY84564.1; -; mRNA.
SQ SEQUENCE 558 AA; 63497 MW; 3CBFD8C829D4CEB8 CRC64;

Query Match 90.7%; Score 2816.5; DB 2; Length 558;
Best Local Similarity 89.8%; Pred. No. 3.2e-150;
Matches 503; Conservative 27; Mismatches 23; Indels 7; Gaps 4;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Db          1 MKTSCAILILMACFGLMNAAVKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNTWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Db        121 EGSEKYSDMVANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTP-TTTPSPTTP----TTTPSPTTPTTTPSPTTPTPTTPTP 475

Db        421 TPTTPSTPSTTTPTPTTPSTPSTTTPTPTTPSTPSTTTPTPTTP-STPSTTTPTPTTPST 479

Qy        476 APTTSTPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVH 535

Db        480 TSTT-TPTPTTTDSTSETPQYTTYVDGHLIKCYKEGDLPHPTNIHKYLVCEYVNGGWWVH 538

Qy        536 IMPCPPGTIWCQEKLTCIGE 555

Db        539 IMPCPPGTIWCQEKLTCITE 558
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RESULT 3
Q4JK69_DERPT
ID Q4JK69_DERPT PRELIMINARY; PRT; 532 AA.
AC Q4JK69;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Group 15 allergen protein short isoform.
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT "Der p 15 0102-An isoform of the gene for Der p15 encoding a chitinase
RT allergen from Dermatophagoides pteronyssinus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; DQ078741; AAY84565.1; -; mRNA.
SQ SEQUENCE 532 AA; 60953 MW; A92BFB6C3C6498ED CRC64;

Query Match 88.3%; Score 2744.5; DB 2; Length 532;
Best Local Similarity 88.3%; Pred. No. 3.3e-146;
Matches 490; Conservative 27; Mismatches 15; Indels 23; Gaps 4;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Db          1 MKTSCAILILMACFGLMNAAVKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNTWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Db        121 EGSEKYSDMVANPTYRKQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
```

```
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              |||||||||||||:|||||||||||||||| ||||||||||||||||:||:||||||||
Db        361 KLAPLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||        |||:|||             ||||:|||| :||| ||||||||:  |:|:
Db        421 TP--------TTPSTPS-------------TTTPTPTTP-STPSTTTPTPTTPS-TPSTT 457

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
              ||:||||: |||||||||||||||||||||:|||||||||||||:||||||||||||||
Db        458 TPTPTTTDSTSETPKYTTYVDGHLIKCYKEGDLPHPTNIHKYLVCEYVNGGWWVHIMPCP 517

Qy        541 PGTIWCQEKLTCIGE 555
              ||||||||||||| |
Db        518 PGTIWCQEKLTCITE 532


RESULT 4
O44079_ANOGA
ID   O44079_ANOGA PRELIMINARY;      PRT;   525 AA.
AC   O44079;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chitinase.
GN   Name=AgChi-1;
OS   Anopheles gambiae (African malaria mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=7165;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Gut;
RX   MEDLINE=98030563; PubMed=9360958; DOI=10.1074/jbc.272.46.28895;
RA   Shen Z., Jacobs-Lorena M.;
RT   "Characterization of a novel gut-specific chitinase gene from the
RT   human malaria vector Anopheles gambiae.";
RL   J. Biol. Chem. 272:28895-28900(1997).
DR   EMBL; AF008575; AAB87764.1; -; mRNA.
DR   PIR; T44445; T44445.
DR   HSSP; Q13231; 1LG2.
DR   Ensembl; ENSANGG00000017996; Anopheles gambiae.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   SMART; SM00494; ChtBD2; 1.
DR   SMART; SM00636; Glyco_18; 1.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS50940; CHIT_BIND_II; 1.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   525 AA;  57211 MW;  3234360EEFF36165 CRC64;

  Query Match             32.5%;  Score 1008.5;  DB 2;  Length 525;
  Best Local Similarity   38.4%;  Pred. No. 1.1e-48;
  Matches  211;  Conservative   93;  Mismatches  187;  Indels   59;  Gaps   13;

Qy          8 LSIMACIGLMNASIKRD-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM 65
                : ::  : :  |:   : |   |     ::|||||||:||   :  | || |||  |||||
Db          5 VGVLVLVAVAAAAFAEEPHKAASAEGKKVVCYVGTWAVYRPGNGRYDIEHIDPSLCTHLM 64

Qy         66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125
              |||  |:|   |::: ||| |   | | :   :|| |:   | | |: ::||| ||| |
Db         65 YGFFGINE-DATVRIIDPYLDLEEN-WGRGHIKRFVGLKNVGPGLKTLAAIGGWNEGSRK 122

Qy        126 YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKD 185
              :| |||:   |::||   : | | : |||:|||||||  | ||| ||: |:  || |:::
Db        123 FSAMAASGELRKRFISDCVAFCQRHGFDGIDLDWEYPAQRDGNPLIDRDNHAQLVEEMRE 182

Qy        186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245
               |: :| ||||||:  :     :|||  ::| | ::||| || || |::: | |||||:
Db        183 EFDHYGLLLTAAVASVEFSAGVSYDIPRISKSFHFLNVMVYDMHGAWDSYCGINAPLYRG 242

Qy        246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
              :| :     ||| ::|::|  | |  |||:|:| ||| :::   :  ::| |  |
Db        243 SADTTDRLGQINVNASIHFWLAQGCTGRKLVLGIPLYGRNFTLASAANTQIGAPTVGGGT 302

Qy        306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL 365
              |  : | ||: | | |:    | | ::: |    ||   :  |||||| |:  |: :|
Db        303 VGRYTREPGVMGYNEFCEKLATEAWDLRWSEEQQVPYAVRNNQWVGYDDLRSVQLKVKYL 362

Qy        366 KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTT 424
              : |: | |||||| ||| | | | : ||:::: :::||           |||||  |:
Db        363 LDQGLGGAMVWSLETDDFLGVCGGGRYPLMHEIRSLVNGGT---------PSTTTMPPSV 413

Qy        425 TPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSP 484
              |||     :| :| | ||||:   | |||  ||  :  |: || : ||     ||  ||
Db        414 APTT-----STVAPGTTTTTPTGANPGTTQPPT--SDAPNHTTTSTTTEGNPGTTRPPSG 466

Qy        485 TTTEHTSETPKYTTYVDGHLIKCY--KEGDIPHPTNIHKYLVC-------EFVNGGWWVH 535
                          ||    |   : | :|||||  :| :|       ||
Db        467 ---------------DG---PCAGGRYGFVPHPTNCARYYICLTADTYYEFT------- 500

Qy        536 IMPCPPGTIW 545
                 |||||::
Db        501 ---CPPGTLP 507


RESULT 5
Q7Q5I7_ANOGA
ID   Q7Q5I7_ANOGA PRELIMINARY;      PRT;   525 AA.
AC   Q7Q5I7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000020485.
GN   ORFNames=ENSANGG00000017996;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008960; EAA10725.2; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
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DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   ProDom; PD000471; Chitinase_II; 1.
DR   SMART; SM00494; ChtBD2; 1.
DR   SMART; SM00636; Glyco_18; 1.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS50940; CHIT_BIND_II; 1.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   525 AA;  56998 MW;  36B4522250257FDF1 CRC64;

  Query Match           32.4%;  Score 1006.5;  DB 2;  Length 525;
  Best Local Similarity   37.1%;  Pred. No. 1.5e-48;
  Matches  204;  Conservative   98;  Mismatches  189;  Indels   59;  Gaps   10;

Qy          8 LSIMACIGLMNASIKRD-HNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLM 65
              : ::  : :  |:   : |   |    ::|||||||:||   :  | || |||  |||||
Db          5 VGVLVLVAVAAAAFAEEPHKAASAEGKKVVCYVGTWAVYRPGNGRYDIEHIDPSLCTHLM 64

Qy         66 YGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEK 125
              |||  |:|   |::: ||| |   | | :   :||  |:   | | |: ::||| ||| |
Db         65 YGFFGINE-DATVRIIDPYLDLEEN-WGRGHIKRFVGLKNVAPGLKTLAAIGGWNEGSRK 122

Qy        126 YSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKD 185
              :| |||:   |::||   : | | : |||:|||||||  | ||| ||: |:  || |:::
Db        123 FSAMAASGELRKRFISDCVAFCQRHGFDGIDLDWEYPAQRDGNPLIDRDNHAQLVEEMRE 182

Qy        186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245
              |: :| ||||||:  :     :|||  ::| | ::||| || || |:::  | |||||:
Db        183 EFDHYGLLLTAAVASVEFSAGVSYDIPRISKSFHFLNVMVYDMHGAWDSYCGINAPLYRG 242

Qy        246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
              :| :     ||| :: ::|  ||  :|||:|:| |||:::: : :  ::| | |
Db        243 SADTTDRLGQMNVNASIQFWLAQGAPAEKLVLGIPLYGRSFTLANAANTQIGAPTVGGGT 302

Qy        306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFL 365
              |  : | ||: | | |:     | | ::: |    ||   :  |:|||| |:  |: :|
Db        303 AGPYTREPGVMGYNEFCEKLATEAWDLRWSEEQQVPYAVRNNQWLGYDDLRSVQLKVKYL 362

Qy        366 KELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTT 424
              : |: | |||||| ||| | | | : ||:::: :::||
Db        363 LDQGLGGAMVWSLETDDFLGVCGGGRYPLMHEIRSLVNGG---------------------- 402

Qy        425 TPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSP 484
                ||:||   ||  : ||| :| | ||||:   | ||  ||:  |   | : ||
Db        403 ---TPSTTTQPPSVASTTTTVAPGTTTTTPTGANPGTTQPPTSDAPNHTTTSTTTGAAPG 459

Qy        485 TTTEHTSETPKYTTYVDGHLIKCY--KEGDIPHPTNIHKYLVC-------EFVNGGWWVH 535
              ||   : : |           |   : | :|||||  :| :|       ||
Db        460 TTQPPSGDGP-----------CAGGRYGFVPHPTNCARYYICLTADTYYEFT------- 500

Qy        536 IMPCPPGTIW 545
                |||||::
Db        501 ---CPPGTLF 507


RESULT 6
Q8ISH5_9ARAC
ID   Q8ISH5_9ARAC PRELIMINARY;      PRT;   431 AA.
AC   Q8ISH5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Chitinase.
OS   Araneus ventricosus.
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
OX   NCBI_TaxID=182803;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15694591; DOI=10.1016/j.cbpc.2004.11.009;
RA   Han J.H., Lee K.S., Li J., Kim I., Je Y.H., Kim D.H., Sohn H.D.,
RA   Jin B.R.;
RT   "Cloning and expression of a fat body-specific chitinase cDNA from the
RT   spider, Araneus ventricosus.";
RL   Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 140:427-435(2005).
DR   EMBL; AY120879; AAN39100.1; -; mRNA.
DR   HSSP; Q13231; 1LG2.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   SMART; SM00636; Glyco_18; 1.
DR   PROSITE; PS01095; CHITINASE_18; UNKNOWN_1.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   431 AA;  47238 MW;  929439397B9BC923 CRC64;

  Query Match           30.3%;  Score 942;  DB 2;  Length 431;
  Best Local Similarity   43.6%;  Pred. No. 5e-45;
  Matches  185;  Conservative   78;  Mismatches  135;  Indels   26;  Gaps    9;

Qy         12 ACIGLM--NASIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGF 68
              ||: |:    ::     | ::   ::|||:|:|: |   :  : || |||| |||::|||
Db          6 ACLLLLLVAVAVSAQSRDRNQKKYKVVCYLGSWANYRGGEGKFLIEHIDPFLCTHVIYGF 65

Qy         69 AKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSD 128
              ||:   :  | |:||| |   | |    ::|||||:  ||:|:|:|::||| ||| |||
Db         66 AKLSNNQ--IAVYDPYLDLKEN-WGLGAFQRFNNLKKTNPQLSTLIAIGGWNEGSTKYSA 122

Qy        129 MAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFE 188
              |||:|  |  |::||:||  :| |||||:|||||  :| |    ||||:: |::|||:||
Db        123 MAADPNARATFVKSVIDFCLKYDFDGLDMDWEYPANR-GGAAHDKQNFVTLLKELKEAFA 181

Qy        189 PHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDE 248
              ||| ||:|||| ||: || ||||  : |  |::||| || || ||   |||||||:|| |
Db        182 PHGLLLSAAVSAGKNTIDTAYDIPGVAKYLDFINVMAYDLHGSWEKTAGHNAPLYERPGE 241

Qy        249 TDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGF 308
              |     ||:| ::|:: ||  ::|:::|:  |||:::: : :   ||    |   |
Db        242 -PESDKILNVDYAINYWIKNGTPKNKVILGMGTYGRSFTLANAANNGLGAATTGPGSAGP 300

Qy        309 ISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKEL 368
              :: | |:| | |:|     : |:  : |   ||| |    |||||  : ||   |: :|
Db        301 LTKEPGMLGYNEIC---SDKGWNEVFVEKVEAPYAYKGNQWVGYDSVKSIGIKVDYLIRE 357

Qy        369 GVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPT 427
              |: | |:|||| |||:|:| | | |||   : : :|||                  ||  |
Db        358 GLGGGMIWSLETDDFRGNCGGGKYPLLTTIASKLNGD-------------VARPTPDPK 403

Qy        428 TPTT 431
                |||
Db        404 QPTT 407


RESULT 7
O17412_AEDAE
ID   O17412_AEDAE PRELIMINARY;      PRT;  1635 AA.
AC   O17412;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Chitinase.
GN   Name=CHT2;
OS   Aedes aegypti (Yellowfever mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Culicinae; Culicini; Aedes; Stegomyia.
OX   NCBI_TaxID=7159;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98324849; PubMed=9662472;
RA   de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
RT   "Chitinases are a multi-gene family in Aedes, Anopheles and
RT   Drosophila.";
RL   Insect Mol. Biol. 7:233-239(1998).
DR   EMBL; AF026492; AAB81850.1; -; Genomic_DNA.
DR   PIR; T14075; T14075.
DR   HSSP; P36222; 1HJX.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 3.
DR   Pfam; PF00704; Glyco_hydro_18; 3.
DR   SMART; SM00494; ChtBD2; 3.
DR   SMART; SM00636; Glyco_18; 3.
DR   PROSITE; PS01095; CHITINASE_18; 3.
DR   PROSITE; PS50940; CHIT_BIND_II; 3.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   1635 AA;  185993 MW;  EA116F83AAC129FA CRC64;

  Query Match             28.0%;  Score 869;  DB 2;  Length 1635;
  Best Local Similarity   34.3%;  Pred. No. 2.9e-40;
  Matches  196;  Conservative   95;  Mismatches  196;  Indels   84;  Gaps   18;

Qy         21 IKRDHNDYSKNPM------RIVCYVGTWSVYHKVD-PYTIEDIDPFKCTHLMYGFAKIDE 73
Db        650 INKETSNQDENAIESDVDYKVVCYFTNWAWYRQGNGKYLPEDIDADLCTHIVYGFAVLDR 709

Qy         74 YKYTIQVFDPYQDDNHNSW---EKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDM 129
Db        710 DRLVIK--------PHDSWADIDNRFYERVVEYKKKGKKVT--VAIGGWNDSAGDKYSRL 759

Qy        130 AANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPK----IDKQNYLALVRELKD 185
Db        760 VRSAAARQKFIADVVAFIEKYGFDGLDLDWEYPVCWQVDCKKGFSDEKEGFASLVVELSQ 819

Qy        186 AFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKR 245
Db        820 AFKPKGLLLSSAVSPSKKVVDEGYDVVTLSDYMDWIAVMAYDYHGQWDKKTGHVAPMYEH 879

Qy        246 PDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSP 305
Db        880 PDDFDKT---FNANFTIHYWIEKGADPRKLVMGMPMYGQSFSLADNKEHGLNAKTYGGGE 936

Qy        306 PGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAF 364
Db        937 AGESTRARGFLSYYEICANIRNKKWTVARDRKGRMGPYAYKGDQWVSFDDQYMIRHKSEY 996

Qy        365 LKELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECIL--GPSTTTPT 421
Db        997 VKAMGLGGAMIWALDLDDFRNLCDCEEYPLLRTINRVLRNYPGPGPRCVLEKEPQREEPR 1056

Qy        422 PTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTST 481
Db       1057 PTRPPTS----------TTPETTRRPSTTTSTRRTTMTTTT--TTTRRPTTTTRRRTSAR 1104

Qy        482 PSPTTTEHTSETPKY---------TTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGW 532
Db       1105 PTYTTT----NVPSYQEIANEVDEPTCTDGRLF-------VPHPTDCNKYYICQYGK--- 1150

Qy        533 WVHIMPCPPGTIW-----------CQEKLT 551
Db       1151 -----LCPGGLYWSVDHCDWPQSTNCRNKQT 1176
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RESULT 8
Q56JI1_9HYME
ID   Q56JI1_9HYME PRELIMINARY;      PRT;   493 AA.
AC   Q56JI1;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Teratocyte released chitinase.
GN   Name=PSP3;
OS   Toxoneuron nigriceps.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
OC   Braconidae; Cardiochilinae; Toxoneuron.
OX   NCBI_TaxID=51531;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Consoli F.L., Lewis D., Keeley L., Vinson S.B.;
RT   "Characterization of a cDNA encoding a putative chitinase from
RT   teratocytes of the endoparasitoid Toxoneuron nigriceps (Hymenoptera,
RT   Braconidae).";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY928055; AAX69085.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   493 AA;  54095 MW;  530F5F86FA95D539 CRC64;

  Query Match             27.8%;  Score 863;  DB 2;  Length 493;
  Best Local Similarity   38.5%;  Pred. No. 1.6e-40;
  Matches  174;  Conservative  100;  Mismatches  152;  Indels   26;  Gaps   11;

Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDIDPFKC 61
Db          5 AIL-LAACVAAAYGSA------ISNQEKKIVCYFGSWAVYRPGRGKFD---IKYIDPTLC 54

Qy         62 THLMYGFAKIDEYKYTIQVFDPYQD--DNHNSWEKRGYERFNNLRLKNPELTTMISLGGW 119
Db         55 THLIYTFTGLN--GDTVKVLDAWQDLPDN---WGKDGFGRFNALREISPSTKTLIAIGGW 109

Qy        120 YEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLAL 179
Db        110 NEGSTKYSKMASDPAARERFADNVVKFIKKWNFDGFDLDWEYPNQRGGSPS-DIENHVEL 168

Qy        180 VRELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHN 239
Db        169 LKALRTRFDKEGLILSAAVAAAESSASKSYKISEVSKYLDFINLMAYDFHGAWESQTGIN 228

Qy        240 APLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDP 299
Db        229 APLRVAAADSGD-YRGWNVESSVNYWLKQGAPKEKLILGVPLYGRAFTLSNPKQNKIGAP 287

Qy        300 AKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASIS 359
Db        288 TRGPGAAGPYTREAGMLGYNEICKMLQKRDWNVIYDEERCAPYAYKDQQWVGFDNIKSIR 347

Qy        360 CKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMI-NGDEKNSFECILG--PS 416
Db        348 EKAQLAKKMDLGGAMIWSVETDDFHGDCGEKYPLLKTLNAVLRGGKEVSNTEDIIGLAEG 407

Qy        417 TTTPTPTTTPTTPTTTPTTPSPTTPTTTPSPT 448
Db        408 SSNNNDDSTASDSTLVNQSDAPASPVIQPTPT 439
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RESULT 9
Q9W2Z3_DROME
ID   Q9W2Z3_DROME PRELIMINARY;      PRT;  4498 AA.
AC   Q9W2Z3;
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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG2989-PA.
GN Name=CG2989; ORFNames=CG2989;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE003449; AAF46544.1; -; Genomic_DNA.
DR HSSP; Q13231; 1LQ0.
DR Ensembl; CG2989; Drosophila melanogaster.
DR FlyBase; FBgn0030171; CG2989.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase_II.
DR InterPro; IPR002557; Chitin_bind_PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS50940; CHIT_BIND_II; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 4498 AA; 493096 MW; AEE65CE0AAB25489 CRC64;

Query Match 27.5%; Score 854.5; DB 2; Length 4498;
Best Local Similarity 33.8%; Pred. No. 5.9e-39;
Matches 202; Conservative 88; Mismatches 188; Indels 119; Gaps 21;

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Qy          2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID 57
              :|:: : ::  ||            |: |    |:|||   ||||     | :|   ::|:
Db         33 QTLFLLCALAYCI----------NEASSEG-RVVCYYTNWSVYRPGTAKFNP---QNIN 77

Qy         58 PFKCTHLMY---GFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMI 114
              |: ||||:|   || | :: |     || |||      |: || :|  |:  | :| |||
Db         78 PYLCTHLVYAFGGFTKDNQMK----PFDKYQD-----IEQGGYAKFTGLKTYNKQLKTMI 128

Qy        115 SLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQ 174
              ::||| | | ::| : |:   |||||:::| ||::  |||:|||||||  | |    |:
Db        129 AIGGWNEASSRFSPLVASNERRQQFIKNILKFLRQNHFDGIDLDWEYPAHREGGKSRDRD 188

Qy        175 NYLALVRELKDAFEPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYD 227
              ||   |:||:  ||           ||| ||  | : ||: ||: :|||  || ||:|||
Db        189 NYAQFVQELRAEFEREAEKTGRTRLLLTMAVPAGIEYIDKGYDVPKLNKYLDWFNVLTYD 248

Qy        228 YHGGWENFYGHNAPLYKRPDETDELHTY---FNVNYTMHYYLNNGATRDKLVMGVPFYGR 284
              :|   |    |:||||    | |  : |    |::|:: |||  || |||||:|:| |||
Db        249 FHSSHEPSVNHHAPLYSL--EEDSEYNYDAELNIDYSIKYYLKAGADRDKLVLGIPTYGR 306

Qy        285 AWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE-EWH-IQYDEYYNAPY 342
              :::: :    :|| ||:|    |  : |:| |:| |:||  : : ||  :| :     ||
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Db        307 SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY 366

Qy        343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMI 401

Db        367 AYRRNQWVGYDDEAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIEAA---- 422

Qy        402 NGDEKNSFECILGPSTTTPTPTTTPTTPTTTPT------------TPSPTT---PTTTP 445

Db        423 ----KEAMVEALGLGINEVAKPSGPQKPSRSRSRDNASNRNRLNGKTEAPLSSRRPSATR 478

Qy        446 SPTTPTTTPSPTTPTTT---------------PSPTTPTPTTPTPAPTTSTPSPTTTEH 489

Db        479 RPAVSSTQAPP--PSTTFKLTEAEGSSLYIGGRASTTPPPPTTPDP------------- 522

Qy        490 TSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNG----GWWVHIMPCPPG 542

Db        523 ------------GSDFKCEEEGFFQHPRDCKKYYWC-LDSGPSGLGIVAHMFTCPSG 566


RESULT 10
Q7PWC2_ANOGA
ID   Q7PWC2_ANOGA PRELIMINARY;      PRT;  2083 AA.
AC   Q7PWC2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000017161 (Fragment).
GN   ORFNames=ENSANGG00000014672;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008984; EAA14807.2; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF01607; CBM_14; 4.
DR   Pfam; PF00704; Glyco_hydro_18; 4.
DR   ProDom; PD000471; Chitinase_II; 4.
DR   SMART; SM00494; ChtBD2; 4.
DR   SMART; SM00636; Glyco_18; 4.
DR   PROSITE; PS01095; CHITINASE_18; 2.
DR   PROSITE; PS50940; CHIT_BIND_II; 4.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
KW   Glycosidase; Hydrolase.
FT   NON_TER       1      1
SQ   SEQUENCE   2083 AA;  234599 MW;  327B7E8B2B644345 CRC64;

  Query Match             27.4%;  Score 851;  DB 2;  Length 2083;
  Best Local Similarity   33.9%;  Pred. No. 3.9e-39;

  Matches  197;  Conservative   92;  Mismatches  192;  Indels  100;  Gaps   18;

Qy         18 NASIKRDHNDYSKNPMRIVCYVGTWSVYHKVD-PYTIEDIDPPKCTHLMYGFAKIDEYKY 76

Db       1172 NESTEVDENSVDSDEYKVVCYFTNWAWYRQGNGKYLPEDIDPDLCTHIVYGFAVLDREGL 1231

Qy         77 TIQVFDPYQDDNHNSW---EKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDMAAN 132

Db       1232 TIK--------PHDSWADIDNRFYERVVELKKKGKKVT--VAIGGWNDSAGDKYSRLVRS 1281

Qy        133 PTYRQQFIQSVLDFLQEYKFDGLDLDWEYP-----GSRLGNPKIDKQNYLALVRELKDAF 187

Db       1282 AQARKRFIDNVMQFIEKYGFDGLDLDWEYPVCWQVDCKKGYAD-EKEGFASLVVELATAF 1340

Qy        188 EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPD 247

Db       1341 KPYGYLLSSAVSPSKKVIDAGYDVRTLSDYMDWIAVMTYDYHGQWDKQTGHVAPMYEHPD 1400

Qy        248 ETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPG 307

Db       1401 DVD---TTFNANFTIHYWIEQGADPRKLVMGMPMYGQSFSLANVNANGLNEKTYGGGEAG 1457

Qy        308 FISGEEGVLSYIELCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAFLK 366

Db       1458 DQTRARGFLSYYEICSNINKKNWNVVRDRKGRMGPYAYKGDQWVSFDDQYMIRHKSEYVK 1517

Qy        367 ELGVSGVMVWSLENDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTT 425

Db       1518 AMGLGGAMIWALDLDDFRNICGCEEYPLLRTINRVLRNYPGPGPKCILG--STKPSPDLS 1575

Qy        426 PTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTT-------------------------- 458

Db       1576 TTRQTTRRTT---TRFSTTSRPTTPSIDDLDSNQSSSKCDGRLFIPHESDCSKYYICQHG 1632

Qy        459 -------PTTT-----------------PSPTTPTP-TTPTPAPTTSTPSPTTTEHTSE 492

Db       1633 KRYEQRCPTNTAWNNGYCDWEENTNCKNKQGPVTSAPSTTEDGSWMTSTSRPTTT----T 1688

Qy        493 TPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWW 533

Db       1689 TPRRTT------TSTTQRGSSDYK------VVCYFTNWAWY 1717


RESULT 11
Q9GQC4_BOMMO
ID   Q9GQC4_BOMMO PRELIMINARY;      PRT;   544 AA.
AC   Q9GQC4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chitinase.
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Shunrei x Showgetsu;
RX   MEDLINE=20545518; PubMed=10984482; DOI=10.1074/jbc.M005271200;
RA   Mikitani K., Sugasaki T., Shimada T., Kobayashi M., Gustafsson J.A.;
RT   "The chitinase gene of the silkworm, Bombyx mori, contains a novel Tc-
RT   like transposable element.";
RL   J. Biol. Chem. 275:37725-37732(2000).
DR   EMBL; AF273695; AAG37105.1; -; mRNA.
DR   HSSP; Q13231; 1LG2.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
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DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   SMART; SM00494; ChtBD2; 1.
DR   SMART; SM00636; Glyco_18; 1.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS50940; CHIT_BIND_II; 1.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   544 AA;  61069 MW;  89872DFC1DA23753 CRC64;

  Query Match             27.3%;  Score 847;  DB 2;  Length 544;
  Best Local Similarity   36.5%;  Pred. No. 1.4e-39;
  Matches  207;  Conservative   78;  Mismatches  218;  Indels   64;  Gaps   19;

Qy          1 MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP 58
              |: |:| |:::| |  |:  :  |          |||||   |:||   |  | ||||
Db          1 MRAIFATLAVLASCAALVQCADSR---------ARIVCYFSNWAVYRPGVGRYGIEDIPV 51

Qy         59 FKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG 118
              ||||:| |  : |    : : ||  |      :| |:  | :|| |:|::  |:::||
Db         52 DLCTHLIYSFIGVTEKSSEVLIIDPELD-----VDKSGFRNFTSLRSKHPDVKFMVAVGG 106

Qy        119 WYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL 177
              | ||  ||| | |  : |  ||:||:|||::| ||||||||||||:   |    ||  :|
Db        107 WAEGGSKYSHMVAQKSTRMSFIRSVVDFLKKYDFDGLDLDWEYPGAADRGGSFSDKDEFL 166

Qy        178 ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF 235
              |:||| ||     |: |||||     ::   | : || :  | ::||:||  | | |
Db        167 YFVQELKRAFIRADRGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGF 226

Qy        236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----- 290
              ::|||||| :    :   |||  :: :   |   :|||:|:|||||::::
Db        227 ADVHSPLYKRPHD-QWAYEKLNVNDGLNLWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY 285

Qy        291 ------RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY 342
                   :  ||||  :  ||       :| |:|     :   |  ::||:   ||
Db        286 GLGTYINKEAGGGDPAPYTNATGF-------WAYYEICTEVDADGSGWTKKWDEFGKCPY 338

Qy        343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
              |    ||||:|  |:  |: ::|| |  | | |::: ||||| || :|||:  :|
Db        339 AYKGTQWVGYEDPRSVEIKMNWIKEKGYLGAMTWAIDMDDFKGLCGEENPLIKLLH---- 394

Qy        403 GDEKNSFECILGPSTT---TPTPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTP 459
              |:     : |: |   ||||     | :||: ||   |     ||| |||  |||
Db        395 ---KHMSTYTVPPARTGHATPTPEW--ARPPSTPSDPSEGDPI----PTTTTTTVKPTTT 445

Qy        460 TTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLIKCYKEGD-IPHPTN 518
              ||  ||  | ||  |  ||           | |     ||   : |  | | :|
Db        446 RTTARPT--TTTTKVPHGTTEEDFDINVRPEVEEPPTENEVDNADV-CNSEDDYVPDKKE 502

Qy        519 IHKYLVCEFVNGGWWVHIMPCPPGTIW 545
              ||  |  |||        | ||||:
Db        503 CSKYWRC--VNGEGVQ--FSCQPGTIF 525


RESULT 12
Q9W2M7_DROME
ID   Q9W2M7_DROME PRELIMINARY;      PRT;   476 AA.
AC   Q9W2M7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG9357-PA.
GN   Name=CG9357; ORFNames=CG9357;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003452; AAF46663.2; -; Genomic_DNA.
DR   HSSP; Q13231; 1GUV.
DR   Ensembl; CG9357; Drosophila melanogaster.
DR   FlyBase; FBgn0034580; CG9357.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006030; P:chitin metabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   ProDom; PD000471; Chitinase_II; 1.
DR   SMART; SM00494; ChtBD2; 1.
DR   SMART; SM00636; Glyco_18; 1.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS50940; CHIT_BIND_II; 1.
KW   Glycosidase; Hydrolase.
SQ   SEQUENCE   476 AA;  52765 MW;  9DECBFCFF3693756 CRC64;

  Query Match           27.1%;  Score 842;  DB 2;  Length 476;
  Best Local Similarity   33.1%;  Pred. No. 2.3e-39;
  Matches  185;  Conservative   94;  Mismatches  182;  Indels   98;  Gaps   11;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPF 59
              |  ::  :: ::  : || ||      |  |||   :||| ||||||   :  : :||||||
Db          1 MWSVSGLVKLLLGVILMAASSSAQGNS-SKN---VVCYQGTWSVYRPGLGKFGMEDIDPF 56

Qy         60 KCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGW 119
               ||||:| |  |:|    ::| | | |   ||  :   : || |:|||| | |::::|||
Db         57 LCTHLIYAFLGIEE-TGQLRVIDAYLDLEENS-GRGNIKSFNALKLKNPVLKTLVAVGGW 114

Qy        120 YEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLAL 179
              |||:::| :| :|: |::|:  |: ||| : |||||||||||| |       |: ||:
Db        115 NEGSKRFSLVARDPSKREKFVDDVVRFLQRHGFDGLDLDWEYPGQRHSLDNEDRSNYITF 174

Qy        180 VRELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHN 239
              ::|||:  || |::|:|||   :   : :|||  :    | :||| || || |:   | |
Db        175 LKELKEGLEPFGFILSAAVGSAQFSAEISYDIPAMVPYLDLINVMAYDLHGPWDQVVGIN 234

Qy        240 APLY---KRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKL 296
              ||||   |   ::       ||:  : |:|  ||  :||::|||||||:::      :
Db        235 APLYAAEKDASDSSGRQQQLNVDAVVKYWLKAGAPAEKLILGVPFYGRSFTLATAEGNQP 294

Qy        297 GDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLA 356
              | |  |    |  | | ||| | |||:: ::|||  :::     || |  : ||||:|
Db        295 GAPHIGKGIAGNYSREPGVLGYNELCEMMEREEWTQKWEATQQVPYAYRQRQWVGYEDPR 354

Qy        357 SISCKLAFLKELGVSGVMVWSLENDDFKGHCGPK-NPLLNKVHNMINGDEKNSFECILGP 415
              |:: |  :: :  : |:|:||||:|||:| || :  |||:::: :: |
Db        355 SLALKAQYVMDNHLGGIMIWSLESDDFRGTCGQQPYPLLHEINRVLFGG---------- 403

Qy        416 STTTPTPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTP 475

Db        404 ---------------------------------------------------------- 403

Qy        476 APTTSTPSPTTTEHTSETPK--YTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWW 533
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                :|||  |||   |:|   ::   |         | |  | |  |:  |     |
Db        404 ----NTPSGLTTESNRESPSEGFSCPADA------PAGYIRDPDNCSKFYYC----SGGK 449

Qy        534 VHIMPCPPGTIWCQEKLTC 552
              |   || |  :  :  :|
Db        450 THNFDCPSGLNFDLDTKSC 468


RESULT 13
Q8MP05_TENMO
ID   Q8MP05_TENMO PRELIMINARY;      PRT;  2838 AA.
AC   Q8MP05;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Chitinase precursor (EC 3.2.1.14).
GN   Name=chit5;
OS   Tenebrio molitor (Yellow mealworm).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC   Tenebrionidae; Tenebrio.
OX   NCBI_TaxID=7067;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Royer V., Fraichard S., Bouhin H.;
RT   "A Novel putative insect Chitinase with multiple catalytic domains :
RT   hormonal regulation during metamorphosis.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ487081; CAD31740.4; -; mRNA.
DR   HSSP; P36222; 1HJX.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0004568; F:chitinase activity; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006032; P:chitin catabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 5.
DR   Pfam; PF00704; Glyco_hydro_18; 5.
DR   SMART; SM00494; ChtBD2; 5.
DR   SMART; SM00636; Glyco_18; 5.
DR   PROSITE; PS01095; CHITINASE_18; 3.
DR   PROSITE; PS50940; CHIT_BIND_II; 5.
KW   Glycosidase; Hydrolase; Signal.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21   2838       chitinase.
SQ   SEQUENCE   2838 AA;  321409 MW;  608B3F2A8E98B9B7 CRC64;

  Query Match           27.1%;  Score 842;  DB 2;  Length 2838;
  Best Local Similarity   32.2%;  Pred. No. 1.8e-38;
  Matches  198;  Conservative   92;  Mismatches  205;  Indels  120;  Gaps   21;

Qy         31 NP---MRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQD 86
              ||    ::|||   |: | :    |   ||||  |||::|||| ::  :  |:  | : |
Db       1919 NPNSEFKVVCYFTNWAWYRQGPGKYLPSDIDPDLCTHIVYGFAVLNGDQLIIKPHDTWAD 1978

Qy         87 DNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGS-EKYSDMAANPTYRQQFIQSVLD 145
                 :: : ||:    : |   :  :|::||| : : :||| :  ||: |::||  |:|
Db       1979 -----FDNKFYEKVTAFKAKG--IKVLIAIGGWNDSAGDKYSRLVNNPSSRRRFIAHVVD 2031

Qy        146 FLQEYKFDGLDLDWEYP-----GSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSP 200
              |::  |||||||||||          | |  || ::   |:|| :|| | |:||:|||||
Db       2032 FIENNNFDGLDLDWEYPKCWQVDCNKG-PASDKSSFAEPVKELHEAFTPKGWLLSAAVSP 2090

Qy        201 GKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNY 260
                :  :|  ||:  |::  ||: || ||||| |:   || ||:|  ||: |     || |:
Db       2091 SRRVVDAGYDVPTLSRYLDWIAVMCYDYHGQWDKITGHVAPMYAHPDDVD---ATFNTNF 2147
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Qy        261 TMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGPISGEEGVLSYIE 320
              |:||::  || | |||||:| ||:::|: | ::  :  |  |    |  :   | ||| |
Db       2148 TIHYWIEKGADRKKLVMGMPMYGQSFSLADNNQNGVNAPTYGGGEAGEETRARGFLSYYE 2207

Qy        321 LCQLFQKEEWHIQYDEYYN-APYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
              :|     : | :  |       || :    || :||:  |  |  |:: :|: | |:|:|:
Db       2208 ICTNVINKGWTVVRDRRGRIGPYAHLRDQWVSFDDIGMIRHKSEFIRAMGLGGGMIWALD 2267

Qy        380 NDDFKGHCG-PKNPLLNKVHNMINGDEKNSFECILGPSTTTPT--PTTTPT-TPTTTPT- 434
               |||:  ||  : |||  :: ::    |   :|||| ::: ||  ||  ||  ||  ||
Db       2268 LDDFRNLCGCEEYPLLRTINRVLRDYAKPDPKCILGKASSKPTQKPTPKPTQKPTPKPTQ 2327

Qy        435 --TPSPTTPTTTP-SPTT------PTTTPSPTTP------------------------- 459
               || |:||   |  |:|       | :| |  |
Db       2328 KPTPKPSTPPYEPQKPSTQKPSYGTTESPEPVMPPDSVPCRGRLFVADEKNCNQYYLCNQ 2387

Qy        460 ------------------------------TTTPSPTTPTPTTPTPAPTTSTPSPTT-- 486
                                           ||| :|:| | |     |   | | |
Db       2388 GELQLQVCPNGLFWNRDHCDWPENTECHPDGTTTAAPSTTTQTLEVEVPEVEVPEPVTTP 2447

Qy        487 ------TEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYL-------VCEFVNGGWW 533
                  |: |   |  |       |::||       |||       :|  :| |:
Db       2448 AAPVGGTDVTEGAYKVVCYFTNW--AWYRQGD-------GKYLPQDIDASLCTHINYGFA 2498

Qy        534 V---HIMPCPPGTIW 545
              |     |   |   |
Db       2499 VLDGSTMTLKPHDSW 2513
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RESULT 14
Q8WR52_BOMMO
ID   Q8WR52_BOMMO PRELIMINARY;      PRT;   566 AA.
AC   Q8WR52;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Chitinase precursor (EC 3.2.1.14).
GN   Name=chiB4;
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Kinshu x Showa; TISSUE=Integument;
RX   MEDLINE=22172809; PubMed=12045191; DOI=10.1074/jbc.M112422200;
RA   Abdel-Banat B.M.A., Koga D.;
RT   "Alternative splicing of the primary transcript generates
RT   heterogeneity within the products of the gene for Bombyx mori
RT   chitinase.";
RL   J. Biol. Chem. 277:30524-30534(2002).
DR   EMBL; AF455139; AAL51080.1; -; mRNA.
DR   HSSP; Q13231; 1LG2.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008061; F:chitin binding; IEA.
DR   GO; GO:0004568; F:chitinase activity; IEA.
DR   GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006032; P:chitin catabolism; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR002557; Chitin_bind_PerA.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   Pfam; PF01607; CBM_14; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   SMART; SM00494; ChtBD2; 1.
DR   SMART; SM00636; Glyco_18; 1.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS50940; CHIT_BIND_II; 1.
KW   Glycosidase; Hydrolase; Signal.
FT   SIGNAL       1     21       Potential.
FT   CHAIN       22    566       chitinase.
SQ   SEQUENCE   566 AA;  63465 MW;  43FC717B3F6917D0 CRC64;

  Query Match           27.0%;  Score 839;  DB 2;  Length 566;
  Best Local Similarity   35.9%;  Pred. No. 4.1e-39;
  Matches  207;  Conservative   78;  Mismatches  209;  Indels   82;  Gaps   20;

Qy          1 MKTIYAILSIMA-CIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDP 58
              |: |:| |:::| |  |:  :  |           |||||   |:||   |  | ||||
Db          1 MRAIFATLAVLASCAALVQCADSR---------ARIVCYFSNWAVYRPGVGRYGIEDIPV 51

Qy         59 FKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGG 118
                ||||:| |  : |    : : ||  |      :| |:  | :|| |:|::  |:::||
Db         52 DLCTHLIYSFIGVTEKSSEVLIIDPELD-----VDKSGFRNFTSLRSKHPDVKFMVAVGG 106

Qy        119 WYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYL 177
              | ||  ||| | |  : |  ||:||:|||::| ||||||||||||:   |    ||  :|
Db        107 WAEGGSKYSHMVAQKSTRMSFIRSVVDFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFL 166

Qy        178 ALVRELKDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENF 235
              |:||| ||     |: |||||     ::   | : || :  | ::||:||  | |  |
Db        167 YFVQELKRAFIRAGRGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGF 226

Qy        236 YGHNAPLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED----- 290
                ::|||||| :    :   |||  :: :   |   :|||:|:|||||::::
Db        227 ADVHSPLYKRPHD-QWAYEKLNVNDGLNLWEEKGCPTNKLVVGIPFYGRSFTLSAGNNNY 285

Qy        291 ------RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE--EWHIQYDEYYNAPY 342
                   :  ||||  :  ||        :| |:|    :   |  ::||:   ||
Db        286 GLGTYINKEAGGGDPAPYTNATGF-------WAYYEICTEVDADGSGWTKKWDEFGKCPY 338

Qy        343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMIN 402
              |    ||||:|  |:  |: ::|| |  | | |::: ||||| || :|||:  :|  ::
Db        339 AYKGTQWVGYEDPRSVEIKMNWIKEKGYLGAMTWAIDMDDFKGLCGEENPLIKLLHKHMS 398

Qy        403 GDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTT----TPSPTTPTTTPSPTT 458
                        : | |   |  ||||     | |:||:       | ||| |||  |||
Db        399 ------------TYTVPPARTGHTTPTPEWARP-PSTPSDPSEGDPIPTTTTTTTVKPTT 444

Qy        459 PTTTPSPTTPTPTTPTPAPTTSTPSPTTTE--------HTSETPKYTTYVDGHLIKCYKE 510
                ||  |||          ||  |  || |           | |    ||   : |  |
Db        445 TRTTARPTT---------TTTKVPHGTTEEDFDINVRPEVEELPT-ENEVDNADV-CNSE 493

Qy        511 GD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIW 545
               | :|      ||  |  |||         | ||||:
Db        494 DDYVPDKKECSKYWRC--VNGEGVQ--FSCQPGTIF 525
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RESULT 15
CHIT_MANSE
ID   CHIT_MANSE     STANDARD;      PRT;   554 AA.
AC   P36362;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Endochitinase precursor (EC 3.2.1.14).
OS   Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;
OC   Sphingidae; Sphinginae; Manduca.
OX   NCBI_TaxID=7130;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93357793; PubMed=8353525; DOI=10.1016/0965-1748(93)90043-R;
RA   Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;
RT   "Sequence of a cDNA and expression of the gene encoding epidermal and
RT   gut chitinases of Manduca sexta.";
RL   Insect Biochem. Mol. Biol. 23:691-701(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97215580; PubMed=9061927; DOI=10.1016/S0965-1748(96)00066-5;
RA   Choi H.K., Choi K.H., Kramer K.J., Muthukrishnan S.;
```

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RT   "Isolation and characterization of a genomic clone for the gene of an
RT   insect molting enzyme, chitinase.";
RL   Insect Biochem. Mol. Biol. 27:37-47(1997).
CC   -!- FUNCTION: Digests chitin in the exoskeleton during the molting
CC       process.
CC   -!- CATALYTIC ACTIVITY: Random hydrolysis of N-acetyl-beta-D-
CC       glucosaminide 1,4-beta-linkages in chitin and chitodextrins.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Epidermis and gut.
CC   -!- DEVELOPMENTAL STAGE: High levels seen in the epidermis on day 0,
CC       but rapidly disappears and is undetected on days 1-4 of fifth
CC       instar. It reappears on day 5 and peaks on day 7 after which a
CC       rapid decline is seen. In the gut is detected on day 6 with lower
CC       levels seen on days 0, 7 and 8.
CC   -!- SIMILARITY: Belongs to the glycosyl hydrolase 18 family. Chitinase
CC       class II subfamily.
CC   -!- SIMILARITY: Contains 1 chitin-binding type-2 domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U02270; AAC04924.1; -; mRNA.
DR   EMBL; L49234; AAB53952.1; -; Genomic_DNA.
DR   PIR; A56596; A56596.
DR   HSSP; Q13231; 1LG2.
DR   InterPro; IPR011583; Chitinase_II.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   InterPro; IPR001579; Glyco_hydro_18AS.
DR   InterPro; IPR002557; PerA_Chitin_bd.
DR   Pfam; PF01607; CBM_14; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   ProDom; PD000471; Chitinase_II; 1.
DR   PROSITE; PS50940; CHIT_BIND_II; 1.
DR   PROSITE; PS01095; CHITINASE_18; 1.
KW   Carbohydrate metabolism; Chitin degradation; Chitin-binding;
KW   Glycoprotein; Glycosidase; Hydrolase; Polysaccharide degradation;
KW   Signal.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    554       Endochitinase.
FT   DOMAIN      495    553       Chitin-binding type-2.
FT   COMPBIAS    396    453       Ser/Thr-rich.
FT   ACT_SITE    146    146       Proton donor (By similarity).
FT   CARBOHYD     85     85       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    407    407       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    545    545       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   554 AA;  62204 MW;  3989D756C96CD490 CRC64;

  Query Match             27.0%;  Score 838.5;  DB 1;  Length 554;
  Best Local Similarity   35.4%;  Pred. No. 4.3e-39;
  Matches  208;  Conservative   79;  Mismatches  210;  Indels   91;  Gaps   20;

Qy          6 AILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHL 64
              | |: :| : |  |          | :  |||||   |:||   |  | ||||   ||||:
Db          3 ATLATLAVLALATAV-------QSDSRARIVCYFSNWAVYRPGVGRYGIEDIPVEKCTHI 55

Qy         65 MYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSE 124
              :| |  : |    : : ||  |      :| |:  | :||  :| :  |:::||| |||
Db         56 IYSFIGVTEGNSEVLIIDPELD-----VDKNGFRNFTSLRSSHPSVKFMVAVGGWAEGSS 110

Qy        125 KYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSR-LGNPKIDKQNYLALVREL 183
              ||| | |  : |  ||:||: ||::| ||||||||||||:   |    ||  :| ||:||
Db        111 KYSHMVAQKSTRMSFIRSVVSFLKKYDFDGLDLDWEYPGAADRGGSFSDKDKFLYLVQEL 170

Qy        184 KDAF--EPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAP 241
              : ||     |: |||||     ::   | : || :  | ::||:||  | | |   ::|
Db        171 RRAFIRVGKGWELTAAVPLANFRLMEGYHVPELCQELDAIHVMSYDLRGNWAGFADVHSP 230

Qy        242 LYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIED---------- 290
              ||||| :    :   |||  :| :   |   :|||:|:|||||::::

Db        231 LYKRPHD-QWAYEKLNVNDGLHLWEEKGCPSNKLVVGIPFYGRSFTLSAGNNNYGLGTFI 289

Qy        291 RSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEE--WHIQYDEYYNAPYGYNDKI 348
                :  ||||   :  ||        :| |:|    |::  |  ::||    || |
Db        290 NKEAGGGDPAPYTNATGF-------WAYYEICTEVDKDDSGWTKKWDEQGKCPYAYKGTQ 342

Qy        349 WVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNS 408
              ||||:|  |:  |: ::|: |  | | |::: |||:| || ||||:  :|  ::
Db        343 WVGYEDPRSVEIKMNWIKQKGYLGAMTWAIDMDDFQGLCGEKNPLIKILHKHMS------ 396

Qy        409 FECILGPSTTTPTPTTTPTTPT-------TTPTTPS-----PTTPTTTPSPTTPTTTPSP 456
                  | | | |  ||||       :||: ||     ||| |  |: || ||  :
Db        397 -------SYTVPPPHTENTTPTPEWARPPSTPSDPSEGDPIPTTTTAKPASTTKTTVKTT 449

Qy        457 TTPTTTPSPTT----------PTP-TTPTPAPTTSTPSPTTTEHTSETPKYTTYVDGHLI 505
              || |  | :           | |   | | |    | ||  |            |||  |
Db        450 TTTTAKPPQSVIDEENDINVRPEPKPEPQPEPEVEVP-PTENE----------VDGSEI 497

Qy        506 KCYKEGD-IPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTC 552
              |  : | ||   :  ||  |  |||         |  ||::  |   |
Db        498 -CNSDQDYIPDKKHCDKYWRC--VNGE--AMQFSCQHGTVFNVELNVC 540


Search completed: March 31, 2006, 15:08:01
Job time : 238 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:19:31 ; Search time 169 Seconds
(without alignments)
1372.161 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3107	100.0	555	4	US-10-218-743-15	Sequence 15, Appl
2	3107	100.0	555	4	US-10-218-743-18	Sequence 18, Appl
3	3014	97.0	536	4	US-10-218-743-21	Sequence 21, Appl
4	2542	81.8	509	4	US-10-218-743-35	Sequence 35, Appl
5	2542	81.8	509	4	US-10-218-743-38	Sequence 38, Appl
6	2475	79.7	490	4	US-10-218-743-41	Sequence 41, Appl
7	854.5	27.5	4498	4	US-10-712-124-68	Sequence 68, Appl
8	854.5	27.5	4498	6	US-11-097-143-2577	Sequence 2577, Ap
9	837.5	27.0	595	6	US-11-097-143-42003	Sequence 42003, A
10	832	26.8	460	6	US-11-097-143-19890	Sequence 19890, A
11	738	23.8	445	4	US-10-004-219B-10	Sequence 10, Appl
12	738	23.8	445	5	US-10-787-845-10	Sequence 10, Appl
13	738	23.8	466	2	US-08-663-618A-2	Sequence 2, Appli
14	738	23.8	466	3	US-09-977-827-4	Sequence 4, Appli
15	738	23.8	466	4	US-10-161-547-2	Sequence 2, Appli
16	738	23.8	466	5	US-10-723-860-1352	Sequence 1352, Ap
17	738	23.8	466	5	US-10-756-149-5051	Sequence 5051, Ap
18	738	23.8	466	6	US-11-063-574A-16	Sequence 16, Appl
19	737.5	23.7	520	4	US-10-268-919-3	Sequence 3, Appli
20	736.5	23.7	473	4	US-10-004-219B-4	Sequence 4, Appli
21	736.5	23.7	473	5	US-10-787-845-4	Sequence 4, Appli
22	735.5	23.7	459	4	US-10-382-248-38	Sequence 38, Appl
23	734.5	23.6	473	6	US-11-063-574A-11	Sequence 11, Appl
24	734.5	23.6	473	6	US-11-063-574A-15	Sequence 15, Appl
25	732.5	23.6	387	3	US-09-977-827-6	Sequence 6, Appli
26	732	23.6	447	4	US-10-382-248-44	Sequence 44, Appl
27	732	23.6	466	2	US-08-663-618A-4	Sequence 4, Appli
28	732	23.6	466	4	US-10-161-547-4	Sequence 4, Appli
29	729.5	23.5	452	4	US-10-004-219B-9	Sequence 9, Appli
30	729.5	23.5	452	5	US-10-787-845-9	Sequence 9, Appli
31	726	23.4	464	6	US-11-063-574A-12	Sequence 12, Appl
32	723	23.3	508	6	US-11-097-143-25989	Sequence 25989, A
33	721.5	23.2	373	2	US-08-663-618A-14	Sequence 14, Appl
34	721.5	23.2	373	2	US-08-663-618A-15	Sequence 15, Appl
35	721.5	23.2	373	4	US-10-161-547-14	Sequence 14, Appl
36	721.5	23.2	373	4	US-10-161-547-15	Sequence 15, Appl
37	710	22.9	484	6	US-11-097-143-3153	Sequence 3153, Ap
38	708.5	22.8	455	4	US-10-004-219B-14	Sequence 14, Appl
39	708.5	22.8	455	5	US-10-787-845-14	Sequence 14, Appl
40	708.5	22.8	455	5	US-10-889-351-1	Sequence 1, Appli
41	708.5	22.8	476	4	US-10-004-219B-1	Sequence 1, Appli
42	708.5	22.8	476	4	US-10-268-919-5	Sequence 5, Appli
43	708.5	22.8	476	5	US-10-787-845-1	Sequence 1, Appli
44	708.5	22.8	476	5	US-10-889-351-5	Sequence 5, Appli
45	705.5	22.7	617	4	US-10-369-493-6743	Sequence 6743, Ap

ALIGNMENTS

RESULT 1
US-10-218-743-15
; Sequence 15, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-15

Query Match 100.0%; Score 3107; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
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Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
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Db        541 PGTIWCQEKLTCIGE 555


RESULT 2
US-10-218-743-18
; Sequence 18, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-18

  Query Match            100.0%;  Score 3107;  DB 4;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 9e-202;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
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Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

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              |||||||||||||||
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RESULT 3
US-10-218-743-21
; Sequence 21, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 536
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-21

  Query Match            97.0%;  Score 3014;  DB 4;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-195;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 439
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 420

Qy        440 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 499
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 480

Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536


RESULT 4
US-10-218-743-35
; Sequence 35, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 509
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-35

  Query Match             81.8%;  Score 2542;  DB 4;  Length 509;
  Best Local Similarity   81.7%;  Pred. No. 1.4e-163;
  Matches  456;  Conservative   24;  Mismatches   26;  Indels   52;  Gaps    2;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
                ||| :|:  | ||||||||: |||||:||||||||||||||||||||||||||||||||||.
Db          1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
                ||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
                ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| ||

Db        121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
                ||||:|||| |||||||||||||| ||::||||:|||||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
                |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
                |||||||||||||:|||||||||||||||| ||||||||||||||||:||:||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
                ||||  || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                  ||||: |||||||||:|||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
                || || |      || |
Db        492 DCPKGTRWHATLKNCIQE 509


RESULT 5
US-10-218-743-38
; Sequence 38, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT:  Hunter, Shirley Wu
;  APPLICANT:  Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/10/218,743
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: US/09/292,225
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/098,909
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/085,295
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,565
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: 09/062,013
;  PRIOR FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
;   LENGTH: 509
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-10-218-743-38

  Query Match             81.8%;  Score 2542;  DB 4;  Length 509;
  Best Local Similarity   81.7%;  Pred. No. 1.4e-163;
  Matches  456;  Conservative   24;  Mismatches   26;  Indels   52;  Gaps    2;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
                ||| :|:  | ||||||||: |||||:||||||||||||||||||||||||||||||||||
Db          1 MKTTFALFCIWACIGLMNAATKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
                ||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWY 120
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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||| ||
Db        121 EGSEKYSDMAANPTYRQQFVQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||:|||| |||||||||||||||| ||::||||:|||||||||||||||||| :||||
Db        181 RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFITGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSPECILGPSTTTP 420
              |||||||||||||:|||||||||||||| ||||||||||||||:||:||||||||
Db        361 KLAFLKELGVSGVMIWSLENDDFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||   || |||||
Db        421 TPTTPSTTSTTTPT---------------------------------------------- 434

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIM 537
                  ||||: |||||||||||:|||||||||:| :||||::|||||||::   |||||||||
Db        435 ---PTTTDSTSETPKYTTYIDGHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIM 491

Qy        538 PCPPGTIWCQEKLTCIGE 555
              || || |      || |
Db        492 DCPKGTRWHATLKNCIQE 509
```

RESULT 6
US-10-218-743-41
; Sequence 41, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-41

Query Match 79.7%; Score 2475; DB 4; Length 490;
Best Local Similarity 82.5%; Pred. No. 4.5e-159;
Matches 443; Conservative 21; Mismatches 21; Indels 52; Gaps 2;

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Qy         22 KRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 81
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 KRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVF 62
```

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Qy         82 DPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQ 141
              ||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||:|
Db         63 DPFQDDNHNSWEKHGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFVQ 122

Qy        142 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVSPG 201
              |||||||||||||||||||||||||||||||||||||| |||||:|||| ||||||||||
Db        123 SVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLTLVRELKEAFEPFGYLLTAAVSPG 182

Qy        202 KDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYT 261
              ||||| ||::||||:|||||||||||||||| :|||||||||||||||||||||||||||
Db        183 KDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNAPLYKRPDETDELHTYFNVNYT 242

Qy        262 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIEL 321
              ||||||||||||||||||||||||||||||:|||||||||||||:||||||||||||||
Db        243 MHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDPAKGMSPPGFITGEEGVLSYIEL 302

Qy        322 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLEND 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        303 CQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMIWSLEND 362

Qy        382 DFKGHCGPKNPLLNKVHNMINGDEKNSPECILGPSTTTPTPTTTPTTPTTTPTTPSPTTP 441
              ||||||||| ||||||||||||||||:||:||||||||||||  || |||||
Db        363 DFKGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTPTPTTPSTTSTTTPT------- 415

Qy        442 TTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTYVD 501
                                                    ||||: |||||||||:|
Db        416 ----------------------------------------PTTTDSTSETPKYTTYID 433

Qy        502 GHLIKCYKEGDIPHPTNIHKYLVCEFV---NGGWWVHIMPCPPGTIWCQEKLTCIGE 555
              ||||||||:| :||||::|||||||::   |||||||||| || || |      || |
Db        434 GHLIKCYKQGYLPHPTDVHKYLVCEYIATPNGGWWVHIMDCPKGTRWHATLKNCIQE 490
```

RESULT 7
US-10-712-124-68
; Sequence 68, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 68
; LENGTH: 4498
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-712-124-68

Query Match 27.5%; Score 854.5; DB 4; Length 4498;
Best Local Similarity 33.8%; Pred. No. 3.2e-48;
Matches 202; Conservative 88; Mismatches 188; Indels 119; Gaps 21;

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Qy          2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID 57
              :|:: : ::  ||           |: |    |:|||   ||||     | :|   ::|:
Db         33 QTLFLLCALAYCI----------NEASSEG-RVVCYYTNWSVYRPGTAKFNP---QNIN 77

Qy         58 PFKCTHLMY---GFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMI 114
              |: ||||:|   || | :: |    || |||      |: || :|  |:  | :| |||
Db         78 PYLCTHLVYAFGGFTKDNQMK----PFDKYQD-----IEQGGYAKFTGLKTYNKQLKTMI 128

Qy        115 SLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQ 174
              ::||| | | ::| : |:   |||||:::| ||::  |||:|||||| | |    |:
Db        129 AIGGWNEASSRFSPLVASNERRQQFIKNILKFLRQNHFDGIDLDWEYPAHREGGKSRDRD 188

Qy        175 NYLALVRELKDAFEPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYD 227
              ||   |:||:  ||           ||| ||  | : ||: ||: :|||  || ||:|||
Db        189 NYAQFVQELRAEFEREAEKTGRTRLLLTMAVPAGIEYIDKGYDVPKLNKYLDWFNVLTYD 248

Qy        228 YHGGWENFYGHNAPLYKRPDETDELHTY---FNVNYTMHYYLNNGATRDKLVMGVPFYGR 284
```

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Db        249 FHSSHEPSVNHHAPLYSL--EEDSEYNYDAELNIDYSIKYYLKAGADRDKLVLGIPTYGR 306

Qy        285 AWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE-EWH-IQYDEYYNAPY 342

Db        307 SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY 366

Qy        343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMI 401

Db        367 AYRRNQWVGYDDEAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIEAA---- 422

Qy        402 NGDEKNSFECILGPSTTTPTPTTTPTTPTTTPT------------TPSPTT---PTTTP 445

Db        423 ----KEAMVEALGLGINEVAKPSGPQKPSRSRSRDNASNRNRLNGKTEAPLSSRRPSATR 478

Qy        446 SPTTPTTTPSPTTPTTT---------------PSPTTPTPTTPTPAPTTSTPSPTTTEH 489

Db        479 RPAVSSTQAPP--PSTTFKLTEAEGSSLYIGGRASTTPPPPTTPDP-------------- 522

Qy        490 TSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNG----GWWVHIMPCPPG 542

Db        523 -----------GSDFKCEEEGFFQHPRDCKKYYWC-LDSGPSGLGIVAHMFTCPSG 566


RESULT 8
US-11-097-143-2577
; Sequence 2577, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2577
;   LENGTH: 4498
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-2577

  Query Match            27.5%;  Score 854.5;  DB 6;  Length 4498;
  Best Local Similarity  33.8%;  Pred. No. 3.2e-48;
  Matches  202;  Conservative   88;  Mismatches  188;  Indels  119;  Gaps   21;

Qy          2 KTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYH----KVDPYTIEDID 57

Db         33 QTLFLLCALAYCI-----------NEASSEG-RVVCYYTNWSVYRPGTAKFNP---QNIN 77

Qy         58 PFKCTHLMY---GFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMI 114

Db         78 PYLCTHLVYAFGGFTKDNQMK----PFDKYQD-----IEQGGYAKFTGLKTYNKQLKTMI 128

Qy        115 SLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQ 174

Db        129 AIGGWNEASSRFSPLVASNERRQQFIKNILKFLRQNHFDGIDLDWEYPAHREGGKSRDRD 188

Qy        175 NYLALVRELKDAFEPHG-------YLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYD 227

Db        189 NYAQFVQELRAEFEREAEKTGRTRLLLTMAVPAGIEYIDKGYDVPKLNKYLDWFNVLTYD 248

Qy        228 YHGGWENFYGHNAPLYKRPDETDELHTY---FNVNYTMHYYLNNGATRDKLVMGVPFYGR 284

Db        249 FHSSHEPSVNHHAPLYSL--EEDSEYNYDAELNIDYSIKYYLKAGADRDKLVLGIPTYGR 306

Qy        285 AWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKE-EWH-IQYDEYYNAPY 342

Db        307 SYTLINEESTELGAPAEGPGEQGDATREKGYLAYYEICQTLKDDPEWTVVQPNANVMGPY 366

Qy        343 GYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHC-GPKNPLLNKVHNMI 401

Db        367 AYRRNQWVGYDDEAIVRKKAEYVVAQGLGGIMFWAIDNDDFRGTCNGKPYPLIEAA---- 422

Qy        402 NGDEKNSFECILGPSTTTPTPTTTPTTPTTTPT------------TPSPTT---PTTTP 445

Db        423 ----KEAMVEALGLGINEVAKPSGPQKPSRSRSRDNASNRNRLNGKTEAPLSSRRPSATR 478

Qy        446 SPTTPTTTPSPTTPTTT---------------PSPTTPTPTTPTPAPTTSTPSPTTTEH 489

Db        479 RPAVSSTQAPP--PSTTFKLTEAEGSSLYIGGRASTTPPPPTTPDP-------------- 522

Qy        490 TSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNG----GWWVHIMPCPPG 542

Db        523 -----------GSDFKCEEEGFFQHPRDCKKYYWC-LDSGPSGLGIVAHMFTCPSG 566


RESULT 9
US-11-097-143-42003
; Sequence 42003, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42003
;   LENGTH: 595
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-42003

  Query Match            27.0%;  Score 837.5;  DB 6;  Length 595;
  Best Local Similarity  35.2%;  Pred. No. 3.6e-48;
  Matches  201;  Conservative   84;  Mismatches  199;  Indels   87;  Gaps   22;
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Qy         29 SKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDD 87
Db         23 SDQASRIVCYFSNWAVYRTGIGRYGLEDVPADLCTHIIYSFIGVNDKSWDVLVIDPELD- 81

Qy         88 NHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFL 147
Db         82 ----VDQGGFSKFTQLKKSNPNVKLEIAVGGWAEGGSKYSQMVAVRDRRQSFIRSVVRFM 137

Qy        148 QEYKFDGLDLDWEYPGS--RLGNPKIDKQNYLALVRELKDAF--EPHGYLLTAAVSPGKD 203
Db        138 KQYNFDGFDLDWEYPGATDRGGNYG-DKDKFLYFVEELRRAFDREGRGWEITMAVPVAKF 196

Qy        204 KIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMH 263
Db        197 RLNEGYHVPELCEALDAIHAMTYDLRGNWAGFADVHSPLYKRKHD-QYAYEKLNVNDGLA 255

Qy        264 YYLNNGATRDKLVMGVPFYGRAWSIEDRSK-LKLG---DPAKGMSPPGFISGEEGVLSYI 319
Db        256 LWEEMGCPANKLVVGVPFYGRTFTLSNSNKNYNMGTYINKEAGGGAPGPYTNASGFLAYY 315

Qy        320 ELC-QLFQKEE-WHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWS 377
Db        316 EICTEVMDKSKGWTVEWDDAGMVPYTYKDTQWVGYENEASIQIKMDFIKQRGYAGAMTWA 375

Qy        378 LENDDFKGHCGPKNPLLNKVH-NMINGDEKNSFECILGPSTTTPTPTTTP----TTPTTT 432
Db        376 IDMDDFHGMCGRKNGLTQILYDNMKN-----------YRVPEPTRQTTPRPEWAKPPAT 423

Qy        433 PTTP------SPTTPTT---------TPSPTTPTTTPS--PTTPTTTPSPTTPTPTTTP-- 473
Db        424 PPNPDEGAVVAPTTSTTKRPKPKPKPTSSPLSPTSAPGPVPTVGSSTPKPTTKKPKKPKK 483

Qy        474 TPAPTTSTPSPTTTEHTSETPKYTTY----------------VDGHLIKCYKEGDIPHP 516
Db        484 TTTTTTTTPAP---EKSTEEPEEVVYPVDPVEPTDPEQPMGPQFDPNEIDCTNRDFVPHP 540

Qy        517 TNIHKYLVCEFVNGGWWVHIMP----CPPGT 543
Db        541 -NCRKYFRC--------VHGKPVEFECKEGT 562
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RESULT 10
US-11-097-143-19890
; Sequence 19890, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19890
; LENGTH: 460
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19890

Query Match 26.8%; Score 832; DB 6; Length 460;
Best Local Similarity 33.7%; Pred. No. 6.1e-48;
Matches 183; Conservative 87; Mismatches 175; Indels 98; Gaps 11;

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Qy         17 MNASIKRDHNDYSKNPMRIVCYVGTWSVYHK-VDPYTIEDIDPFKCTHLMYGFAKIDEYK 75
Db          1 MAASSSAQGNS-SKN---VVCYQGTWSVYRPGLGKFGMEDIDPFLCTHLIYAFLGIEE-T 55

Qy         76 YTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTY 135
Db         56 GQLRVIDAYLDLEENS-GRGNIKSFNALKLKNPVLKTLVAVGGWNEGSKRFSLVARDPSK 114

Qy        136 RQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLT 195
Db        115 REKFVDDVVRFLQRHGFDGLDLDWEYPGQRHSLDNEDRSNYITFLKELKEGLEPFGFILS 174

Qy        196 AAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLY---KRPDETDEL 252
Db        175 AAVGSAQFSAEISYDIPAMVPYLDLINVMAYDLHGPWDQVVGINAPLYAAEKDASDSSGR 234

Qy        253 HTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGE 312
Db        235 QQQLNVDAVVKYWLKAGAPAEKLILGVPFYGRSFTLATAEGNQPGAPHIGKGIAGNYSRE 294

Qy        313 EGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSG 372
Db        295 PGVLGYNELCEMMEREEWTQKWEATQQVPYAYRQRQWVGYEDPRSLALKAQYVMDNHLGG 354

Qy        373 VMVWSLENDDFKGHCGPK-NPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTPTT 431
Db        355 IMIWSLESDDFRGTCGQQPYPLLHEINRVLFGG-------------------------- 387

Qy        432 TPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTS 491
Db        388 ----------------------------------------------NTPSGLTTESNR 399

Qy        492 ETPK--YTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEK 549
Db        400 ESPSEGFSCPADA------PAGYIRDPDNCSKFYYC----SGGKTHNFDCPSGLNFDLDT 449

Qy        550 LTC 552
Db        450 KSC 452
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RESULT 11
US-10-004-219B-10
; Sequence 10, Application US/10004219B
; Publication No. US20030087414A1
; GENERAL INFORMATION:
; APPLICANT: Macrozyme
; APPLICANT: Aerts, Johannes M.F.G.
; APPLICANT: Boot, Rolf G.
; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
; TITLE OF INVENTION: its use in therapy or prophylaxis against diseases in
; TITLE OF INVENTION: which mucus is involved or infection diseases
; FILE REFERENCE: 2183-5136US
; CURRENT APPLICATION NUMBER: US/10/004,219B
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE

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;   LOCATION: (1)..(445)
;   OTHER INFORMATION: /note="Human chitotriosidase"
US-10-004-219B-10

  Query Match             23.8%;  Score 738;  DB 4;  Length 445;
  Best Local Similarity   34.2%;  Pred. No. 1.3e-41;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
              ::|||   |: | : :  :  :|:||  ||||:| || :  :: :              |
Db          2 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 50

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
               ::  |: || |:  ||:| |::::||| |::|::|| |    || |: | : ||::|
Db         51 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 110

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
              |||||||||||||: |:| :||: :  ||::| :||:           ||:|||  |:
Db        111 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 169

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
              :|  |:: :: :  |::|:| ||:|| ||   |||:|||| :|:    :  ||:  :
Db        170 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 228

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
              :|  |    ||::|:| |||::::   |  ::| || |   ||  : | |:|:| |:|
Db        229 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 288

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
              :  || |:    || : |  |||:||: |   |:::||: |: | |||:|: |||
Db        289 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 345

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
              |                       | |  |          |   |       | |: |
Db        346 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 373

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
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Db        374 PELEVP-KPGQPSEPEHGPSPGQDT 397


RESULT 12
US-10-787-845-10
; Sequence 10, Application US/10787845
; Publication No. US20040253224A1
; GENERAL INFORMATION:
;  APPLICANT: Macrozyme
;  APPLICANT:  Aerts, Johannes M.F.G.
;  APPLICANT:  Boot, Rolf G.
;  TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
;  TITLE OF INVENTION:  its use in therapy or prophylaxis against diseases in
;  TITLE OF INVENTION:  which mucus is involved or infection diseases
;  FILE REFERENCE: 2183-5136US
;  CURRENT APPLICATION NUMBER: US/10/787,845
;  CURRENT FILING DATE:  2004-02-26
;  PRIOR APPLICATION NUMBER: US/10/004,219
;  PRIOR FILING DATE: 2001-11-02
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(445)
;   OTHER INFORMATION: /note="Human chitotriosidase"
US-10-787-845-10

  Query Match             23.8%;  Score 738;  DB 5;  Length 445;
  Best Local Similarity   34.2%;  Pred. No. 1.3e-41;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
              ::|||   |: | : :  :  :|:||  ||||:| || :  :: :              |
Db          2 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 50

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
               ::  |: || |:  ||:| |::::||| |::|::|| |    || |: | : ||::|
Db         51 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 110

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
              |||||||||||||: |:| :||: :  ||::| :||:           ||:|||  |:
Db        111 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 169

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
              :|  |:: :: :  |::|:| ||:|| ||   |||:|||| :|:    :  ||:  :
Db        170 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 228

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
              :|  |    ||::|:| |||::::   |  ::| || |   ||  : | |:|:| |:|
Db        229 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 288

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
              :  || |:    || : |  |||:||: |   |:::||: |: | |||:|: |||
Db        289 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 345

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
              |                       | |  |          |   |       | |: |
Db        346 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 373

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
              |    |     |: |   |||   |
Db        374 PELEVP-KPGQPSEPEHGPSPGQDT 397


RESULT 13
US-08-663-618A-2
; Sequence 2, Application US/08663618A
; Publication No. US20030017570A1
;  GENERAL INFORMATION:
;    APPLICANT:  Gray, Patrick W.
;    TITLE OF INVENTION:  Chitinase Materials and Methods
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/663,618A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rin-Laures, Li-Hsien
;      REGISTRATION NUMBER:  33,547
;      REFERENCE/DOCKET NUMBER:  27866/32960
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  466 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-663-618A-2
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  Query Match             23.8%;  Score 738;  DB 2;  Length 466;
  Best Local Similarity   34.2%;  Pred. No. 1.4e-41;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
              ::|||    |: | : :  :  :|:||  ||||:| || :  :: :              |
Db         23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 71

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
               ::  |: || |:  ||:| |::::||| |::|::|| |    || |: | : ||::|
Db         72 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 131

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
              |||||||||||||: |:| :||: :  ||::| :||:           ||:|||  |:
Db        132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 190

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
              :|  |:: :: :  |::|:| ||:|| ||   |||:||||| :|:    :  ||:  :
Db        191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
              :|  |    ||::|:| |||::::   |  ::| || |   ||  : | |:|:| |:|
Db        250 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 309

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                  :  || |:    || : |  |||:||: |   |:::||: |: | |||:|: |||
Db        310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
              |                      | |  |           |   |       |  |: |
Db        367 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 394

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
              |    |     |: |   |||   |
Db        395 PELEVP-KPGQPSEPEHGPSPGQDT 418


RESULT 14
US-09-977-827-4
; Sequence 4, Application US/09977827
; Publication No. US20020086008A1
; GENERAL INFORMATION:
;  APPLICANT: Aerts, Johannes Maria  F.G.
;  TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decomp
;  TITLE OF INVENTION:  chitin, its use in therapy or prophylaxis against infectious dis
;  FILE REFERENCE: Docket 294-32 DIVII/CON
;  CURRENT APPLICATION NUMBER: US/09/977,827
;  CURRENT FILING DATE:  2001-10-15
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-977-827-4

  Query Match             23.8%;  Score 738;  DB 3;  Length 466;
  Best Local Similarity   34.2%;  Pred. No. 1.4e-41;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
              ::|||    |: | : :  :  :|:||  ||||:| || :  :: :              |
Db         23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 71

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
               ::  |: || |:  ||:| |::::||| |::|::|| |    || |: | : ||::|
Db         72 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 131

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
              |||||||||||||: |:| :||: :  ||::| :||:           ||:|||  |:
Db        132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 190

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
              :|  |:: :: :  |::|:| ||:|| ||   |||:||||| :|:    :  ||:  :
Db        191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
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Db        250 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 309

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                  :  || |:    || : |  |||:||: |   |:::||: |: | |||:|: |||
Db        310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
              |                      | |  |           |   |       |  |: |
Db        367 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 394

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
              |    |     |: |   |||   |
Db        395 PELEVP-KPGQPSEPEHGPSPGQDT 418


RESULT 15
US-10-161-547-2
; Sequence 2, Application US/10161547
; Publication No. US20030143216A1
; GENERAL INFORMATION:
;  APPLICANT: Gray, Patrick W.
;  APPLICANT:  Tjoelker, Larry W.
;  TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
;  FILE REFERENCE: 27866/35407
;  CURRENT APPLICATION NUMBER: US/10/161,547
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: US/09/267,574
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/039,198
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 466
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-161-547-2

  Query Match             23.8%;  Score 738;  DB 4;  Length 466;
  Best Local Similarity   34.2%;  Pred. No. 1.4e-41;
  Matches  152;  Conservative   85;  Mismatches  150;  Indels   58;  Gaps   11;

Qy         34 RIVCYVGTWSVYHKVDP-YTIEDIDPFKCTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSW 92
              ::|||    |: | : :  :  :|:||  ||||:| || :  :: :              |
Db         23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLST----------TEW 71

Qy         93 -EKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
               ::  |: || |:  ||:| |::::||| |::|::|| |    || |: | : ||::|
Db         72 NDETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS 131

Qy        152 FDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHG-------YLLTAAVSPGKDK 204
              |||||||||||||: |:| :||: :  ||::| :||:           ||:|||  |:
Db        132 FDGLDLDWEYPGSQ-GSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTY 190

Qy        205 IDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVNYTMHY 264
              :|  |:: :: :  |::|:| ||:|| ||   |||:||||| :|:    :  ||:  :
Db        191 VDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAAS-LNVDAAVQQ 249

Qy        265 YLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQL 324
              :|  |    ||::|:| |||::::   |  ::| || |   ||  : | |:|:| |:|
Db        250 WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW 309

Qy        325 FQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFK 384
                  :  || |:    || : |  |||:||: |   |:::||: |: | |||:|: |||
Db        310 KGATKQRIQ-DQ--KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFA 366

Qy        385 GHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPTTPTTT 444
              |                      | |  |           |   |       |  |: |
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Db        367 G----------------------FSCNQG---------RYPLIQTLRQELSLPYLPSGT 394

Qy        445 PSPTTPTTTPSPTTPTTTPSPTTPT 469
              |    |.    |: |   |||   |
Db        395 PELEVP-KPGQPSEPEHGPSPGQDT 418
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Search completed: March 31, 2006, 15:23:09
Job time : 171 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:20:29 ; Search time 24 Seconds
(without alignments)
703.969 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 3107
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	534.5	17.2	595	6	US-10-510-386-240	Sequence 240, App
2	259	8.3	5179	7	US-11-108-172-1068	Sequence 1068, Ap
3	216.5	7.0	548	7	US-11-052-554A-324	Sequence 324, App
4	204	6.6	941	7	US-11-169-232-14	Sequence 14, Appl
5	204	6.6	1022	7	US-11-169-232-84	Sequence 84, Appl
6	204	6.6	1038	7	US-11-169-232-74	Sequence 74, Appl
7	204	6.6	1049	7	US-11-169-232-58	Sequence 58, Appl
8	204	6.6	1140	7	US-11-169-232-104	Sequence 104, App
9	204	6.6	1270	7	US-11-169-232-44	Sequence 44, Appl
10	204	6.6	1311	7	US-11-169-232-42	Sequence 42, Appl
11	204	6.6	1313	7	US-11-169-232-142	Sequence 142, App
12	204	6.6	1314	7	US-11-169-232-50	Sequence 50, Appl
13	204	6.6	1320	7	US-11-169-232-46	Sequence 46, Appl
14	204	6.6	1320	7	US-11-169-232-60	Sequence 60, Appl
15	204	6.6	1354	7	US-11-169-232-48	Sequence 48, Appl
16	204	6.6	1361	7	US-11-169-232-40	Sequence 40, Appl
17	204	6.6	1363	7	US-11-169-232-52	Sequence 52, Appl
18	204	6.6	1404	7	US-11-169-232-2	Sequence 2, Appli
19	204	6.6	1404	7	US-11-169-232-62	Sequence 62, Appl
20	191.5	6.2	681	7	US-11-096-568A-2501	Sequence 2501, Ap
21	191.5	6.2	694	7	US-11-096-568A-29818	Sequence 29818, A
22	191.5	6.2	717	7	US-11-096-568A-28799	Sequence 28799, A
23	190.5	6.1	1970	6	US-10-821-234-1641	Sequence 1641, Ap
24	188	6.1	2011	7	US-11-080-991-56	Sequence 56, Appl
25	177.5	5.7	364	7	US-11-087-177-31	Sequence 31, Appl
26	176.5	5.7	364	7	US-11-087-177-33	Sequence 33, Appl
27	170	5.5	359	6	US-10-055-877-265	Sequence 265, App
28	170	5.5	359	7	US-11-080-091-1	Sequence 1, Appli
29	170	5.5	359	7	US-11-116-939-15	Sequence 15, Appl
30	170	5.5	359	7	US-11-087-177-23	Sequence 23, Appl
31	169	5.4	346	7	US-11-036-256-33	Sequence 33, Appl
32	168	5.4	200	7	US-11-036-256-27	Sequence 27, Appl
33	168	5.4	228	7	US-11-036-256-31	Sequence 31, Appl
34	168	5.4	365	7	US-11-087-177-27	Sequence 27, Appl
35	167	5.4	190	7	US-11-096-568A-631	Sequence 631, App
36	167	5.4	209	7	US-11-096-568A-630	Sequence 630, App
37	167	5.4	647	7	US-11-087-099-7887	Sequence 7887, Ap
38	166	5.3	359	7	US-11-087-177-29	Sequence 29, Appl
39	165	5.3	359	7	US-11-087-177-25	Sequence 25, Appl
40	164	5.3	626	7	US-11-010-748A-1	Sequence 1, Appli
41	163.5	5.3	619	6	US-10-517-939-352	Sequence 352, App
42	161	5.2	339	7	US-11-096-568A-21709	Sequence 21709, A
43	161	5.2	341	7	US-11-096-568A-21708	Sequence 21708, A
44	161	5.2	411	7	US-11-036-256-89	Sequence 89, Appl
45	159.5	5.1	493	7	US-11-096-568A-11657	Sequence 11657, A

ALIGNMENTS

RESULT 1
US-10-510-386-240
; Sequence 240, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 240
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-240

Query Match 17.2%; Score 534.5; DB 6; Length 595;
Best Local Similarity 27.5%; Pred. No. 2.3e-30;
Matches 169; Conservative 89; Mismatches 200; Indels 157; Gaps 29;

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Qy          7 ILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMY 66
              |  :|  :  :|  : :   |  ||  :|: |  :|  | :   : : |:|  | :|: |
Db         15 IFVMMLSLSFVNGEVAK--ADSGKN-YKIIGYYPSWGAYGR--DFQVWDMDVSKVSHINY 69

Qy         67 GFAK----------------------------IDEYKYTIQVFDPYQDDNHNS----WEK 94
                ||                            ||   || : ||: |    ::     |::
Db         70 AFADICWEGRHGNPDPTGPNPQTWSCQDENGVIDAPNGTIVMGDPWIDAQKSNPGDVWDE 129

Qy         95 --RG-YERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQFIQSVLDFLQEYK 151
                 || :::   |:  :| | | ||:|||   | ::||:||:|  |: |  | ::||::|
Db        130 PIRGNFKQLLKLKKSHPHLKTFISVGGW-TWSNRFSDVAADPAARENFAASAVEFLRKYG 188

Qy        152 FDGLDLDWEYP--GSRLGN---PKIDKQNYLALVRELK------DAFEPHGYLLTAAVSP 200
              |||:|||||||  |   ||   |: ||:||  |::|::      :| :   ||||  |
Db        189 FDGVDLDWEYPVSGGLPGNSTRPE-DKRNYTLLLQEVRKKLDAAEAKDGKEYLLTIASGA 247

Qy        201 GKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETD----ELHTYF 256
              | :    :: :: :  ||:|:||||::|||::   |||||:  |  :        ||
Db        248 SPDYVSNT-ELDKIAQTVDWINIMTYDFNGGWQSISAHNAPLFYDPKAKEAGVPNAETY- 305

Qy        257 NVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGF-------- 308
              |:  |:  |   |  ||||:| ||||| ||               |  | |
```

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Db        306 NIENTVKRYKEAGVKGDKLVLGTPFYGRGWS-------------GCEPGGHGEYQKCGP 351

Qy        309 ---ISGEEGVLSYIELCQLFQKEEWHIQYDEYYN----APYGYN--DKIWVGYDDLASIS 359
              : |:||  : :| : :  :     |  |:|     |: ||  :  :: |||  |
Db        352 AKEGTWEKGVFDFSDLERNYVNQN---GYKRYWNDQAKVPFLYNAENGNFITYDDEQSFG 408

Qy        360 CKLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTT 419
               |  |:|  |:|| | |     || |       ||||:          : :    |
Db        409 HKTDFIKANGLSGAMFW-----DFSG--DSNRTLLNKL----------AADLDFAPDGGN 451

Qy        420 PTPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSP---------------------- 456
               | |      |:: |      |  | | | :     ||
Db        452 PEP------PSSAPVNVRVTGKTAT-SVSLAWDAPSSGANIAEYVVSFENRSISVKETSA 504

Qy        457 ----TTPTTTPSPTTPTPTT-------PTPAPTTSTPSPTTTEHTSETPKYT----TYVD 501
                  |  | |              ||   ||::    : :   ||  ||       :
Db        505 EIGGLKPGTAYSFTVSAKDADGKLHAGPTVEVTTNSDQACSYDEWKETSAYTGGERVAFN 564

Qy        502 GHL--IKCYKEGDIP 514
               | :   | : :|| |
Db        565 GKVYEAKWWTKGDRP 579
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RESULT 2
US-11-108-172-1068
; Sequence 1068, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1068
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1068

Query Match 8.3%; Score 259; DB 7; Length 5179;
Best Local Similarity 30.4%; Pred. No. 1e-09;
Matches 86; Conservative 18; Mismatches 45; Indels 134; Gaps 13;

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Qy        280 PFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQY----- 334
              || |   : ||     : ||                  :: | |  || :  :
Db       1325 PFDGVCGAPEDIECRSVKDP-----------------HLSLEQHGQKVQCDVSVGFICK 1366

Qy        335 --DEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLENDDFKGHCGPKNP 392
                |:: | |:|      : ||    ::|                              | | :
Db       1367 NEDQFGNGPFG------LCYDYKIRVNC-------------------------CWPMD- 1393

Qy        393 LLNKVHNMINGDEKNSFECILGPS--TTTPT----------PTTTPTTPTTTPTTPSPTT 440
                          :||  ||  ||||:          |||||: |||| ||| |||
Db       1394 ----------------KCITTPSPPTTTPSPPPTTTTTLPPTTTPSPPTTTTTTPPPTT 1436

Qy        441 ------------PTTTPSP-----TT--PTTTPSPTT-----PTTTPSPTTPTPTTPTP 475
                         |||||||     ||  ||||||| |      |||||| | | ||| |
Db       1437 TPSPPITTTTTPLPTTTPSPPISTTTTPPPTTTPSPPTTTPSPPTTTPSPPTTTTTTPPP 1496

Qy        476 A-------------------PTTSTPSPTTTEHTSETPKYTT 498
                                  | |:|||| ||  |: ||  ||
Db       1497 TTTPSPPMTTPITPPASTTTLPPTTTPSPPTT--TTTTPPPTT 1537
```

RESULT 3
US-11-052-554A-324
; Sequence 324, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 324
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-324

Query Match 7.0%; Score 216.5; DB 7; Length 548;
Best Local Similarity 54.3%; Pred. No. 6.6e-08;
Matches 51; Conservative 3; Mismatches 23; Indels 17; Gaps 5;

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Qy        416 STTTPTPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPT---------TTPSPT 466
              | ||| ||| |||| ||| |  |||| ||| |||| |||  | ||         || :||
Db        423 SATTP-PTTPPTTPVTTPPTTPPTTPVTTP-PTTPPTTPVTTPPTTVAPTTVAPTTVAPT 480

Qy        467 TPTPTTPTPA---PTTSTPSPT---TTEHTSETP 494
              |  |||  ||   |||  | ||   | : | : |
Db        481 TVAPTTVAPATATPTTVAPQPTQQPTQQPTQQMP 514
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RESULT 4
US-11-169-232-14
; Sequence 14, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.

```
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 941 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-169-232-14

  Query Match             6.6%;  Score 204;  DB 7;  Length 941;
  Best Local Similarity   41.8%;  Pred. No. 9.8e-07;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        534 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 593

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        594 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 649

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |      || |||
Db        650 TPPPTT----------SEVSTPTTTKEPTTIHK 672


RESULT 5
US-11-169-232-84
; Sequence 84, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 84:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1022 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-11-169-232-84

  Query Match             6.6%;  Score 204;  DB 7;  Length 1022;
  Best Local Similarity   41.8%;  Pred. No. 1.1e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        615 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 674

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        675 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 730

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |      || |||
Db        731 TPPPTT----------SEVSTPTTTKEPTTIHK 753


RESULT 6
US-11-169-232-74
; Sequence 74, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
```

```
;                 Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 74:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1038 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-11-169-232-74

  Query Match             6.6%;  Score 204;  DB 7;  Length 1038;
  Best Local Similarity   41.8%;  Pred. No. 1.1e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        599 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 658

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        659 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 714

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |     || |||
Db        715 TPPPTT----------SEVSTPTTTKEPTTIHK 737


RESULT 7
US-11-169-232-58
; Sequence 58, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1049 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-11-169-232-58

  Query Match             6.6%;  Score 204;  DB 7;  Length 1049;
  Best Local Similarity   41.8%;  Pred. No. 1.1e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        642 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 701

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        702 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 757

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |     || |||
Db        758 TPPPTT----------SEVSTPTTTKEPTTIHK 780


RESULT 8
US-11-169-232-104
; Sequence 104, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
```

```
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 104:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1140 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-11-169-232-104

  Query Match             6.6%;  Score 204;  DB 7;  Length 1140;
  Best Local Similarity   41.8%;  Pred. No. 1.2e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||      |||  |:||||     |||  | |||   |:||
Db        733 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 792

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        793 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 848

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |      || |||
Db        849 TPPPTT----------SEVSTPTTTKEPTTIHK 871


RESULT 9
US-11-169-232-44
; Sequence 44, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 44:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1270 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-11-169-232-44

  Query Match             6.6%;  Score 204;  DB 7;  Length 1270;
  Best Local Similarity   41.8%;  Pred. No. 1.4e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||      |||  |:||||     |||  | |||   |:||
Db        599 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 658

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        659 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 714

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |      || |||
Db        715 TPPPTT----------SEVSTPTTTKEPTTIHK 737


RESULT 10
US-11-169-232-42
; Sequence 42, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
```

```
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 42:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1311 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-11-169-232-42

  Query Match             6.6%;  Score 204;  DB 7;  Length 1311;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        640 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 699

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        700 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 755

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||          |   |      || |||
Db        756 TPPPTT----------SEVSTPTTTKEPTTIHK 778


RESULT 11
US-11-169-232-142
; Sequence 142, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 142:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1313 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-11-169-232-142

  Query Match             6.6%;  Score 204;  DB 7;  Length 1313;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        642 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 701

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        702 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 757

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||          |   |      || |||
Db        758 TPPPTT----------SEVSTPTTTKEPTTIHK 780


RESULT 12
US-11-169-232-50
; Sequence 50, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
```

```
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;    INFORMATION FOR SEQ ID NO: 50:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1314 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-11-169-232-50

  Query Match             6.6%;  Score 204;  DB 7;  Length 1314;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        643 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 702

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        703 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 758

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |     || |||
Db        759 TPPPTT----------SEVSTPTTTKEPTTIHK 781


RESULT 13
US-11-169-232-46
; Sequence 46, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;    INFORMATION FOR SEQ ID NO: 46:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1320 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-11-169-232-46

  Query Match             6.6%;  Score 204;  DB 7;  Length 1320;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        649 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 708

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        709 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 764

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |     || |||
Db        765 TPPPTT----------SEVSTPTTTKEPTTIHK 787


RESULT 14
US-11-169-232-60
; Sequence 60, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
```

```
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;    INFORMATION FOR SEQ ID NO: 60:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1320 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-11-169-232-60

  Query Match             6.6%;  Score 204;  DB 7;  Length 1320;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
              | |:||  || ||:    ||||     |||  |:||||     |||  | |||   |:||
Db        649 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 708

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        709 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 764

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
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Db        765 TPPPTT----------SEVSTPTTTKEPTTIHK 787


RESULT 15
US-11-169-232-48
; Sequence 48, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;    INFORMATION FOR SEQ ID NO: 48:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1354 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-11-169-232-48

  Query Match             6.6%;  Score 204;  DB 7;  Length 1354;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-06;
  Matches   64;  Conservative    6;  Mismatches   25;  Indels   58;  Gaps   12;

Qy        413 LGPSTT-TPTPTTT----PTTP----TTTPTTPSPTTP----TTTPSPTTPTT--TPSPT 457
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Db        683 LAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 742

Qy        458 T----------PTTT----------PSPTTPTPTTPT----PAPTT-STPSPTTTEHTSE 492
              |          ||||          |:||||  | ||    |||||   |:||    | |
Db        743 TPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPT----TPE 798

Qy        493 TPKYTTYVDGHLIKCYKEGDIP----HPTNIHK 521
              ||  ||           |   |     || |||
Db        799 TPPPTT----------SEVSTPTTTKEPTTIHK 821


Search completed: March 31, 2006, 15:23:39
Job time : 25 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:23:24 ; Search time 190 Seconds
(without alignments)
1283.449 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 3 35

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	555	100.0	555	3	AAY52523	Aay52523 House dus
2	555	100.0	555	5	AAU96327	Aau96327 Der HMW-m
3	555	100.0	555	5	AAU96328	Aau96328 Der HMW-m
4	536	96.6	536	3	AAY52525	Aay52525 House dus
5	536	96.6	536	5	AAU96329	Aau96329 Der HMW-m
6	64	11.5	490	3	AAY52535	Aay52535 D. pteron
7	64	11.5	490	5	AAU96339	Aau96339 Der HMW-m
8	64	11.5	509	3	AAY52533	Aay52533 D. pteron
9	64	11.5	509	5	AAU96337	Aau96337 Der HMW-m
10	64	11.5	509	5	AAU96338	Aau96338 Der HMW-m

ALIGNMENTS

RESULT 1
AAY52523
ID AAY52523 standard; protein; 555 AA.
XX
AC AAY52523;
XX
DT 22-FEB-2000 (first entry)
XX
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.
XX
OS Dermatophagoides farinae.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /note= "Signal peptide"
FT Protein 20. .555
FT /note= "Mature PDerf98-555"
XX
PN WO9954349-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2000-052700/04.
DR N-PSDB; AAZ38575, AAZ38576, AAZ38577, AAZ38578.
XX
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivy to mite allergens.
XX
PS Claim 3; Page 111-113; 154pp; English.
XX
CC This sequence represents Dermatophagoides farinae mite allergen protein
CC (map) PDerf98-555. PDerf98-555 has a molecular weight of 98 kD,
CC comprising 555 amino acids, and is a component of the Dermatophagoides
CC farinae high molecular weight mite allergen protein (HWM-map)
CC composition. The HMW-map composition was isolated from a D. farinae
CC homogenate by gel filtration, with each fraction being analysed for the
CC presence of proteins that bound to IgE present in mite-allergic dog
CC antisera. Mite allergenic proteins and peptides, and nucleic acids
CC encoding them, may be used in therapeutic compositions to modify an
CC animal's hypersensitivity reaction to mite allergens. Animals that may be
CC treated include mammals and birds, especially felines, canines, equines,
CC humans, other pets, and work or domestic animals. The proteins or
CC fragments may also be used to diagnose allergies via a skin test. The
CC proteins and peptides can also be used to raise antibodies, which have a
CC variety of potential uses. For example, they can be used as vaccines to
CC passively immunise animals against dust mite hypersensitivity, as
CC positive controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 555; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
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Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYBRFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
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Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
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RESULT 2
AAU96327
ID AAU96327 standard; protein; 555 AA.
XX
AC AAU96327;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #14.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69571.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 114-116; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 555 AA;

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  Query Match             100.0%;  Score 555;  DB 5;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
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Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
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Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
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Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
```

RESULT 3
AAU96328
ID AAU96328 standard; protein; 555 AA.
XX
AC AAU96328;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #15.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX

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PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028730.
XX
PR   14-SEP-2000; 2000US-00662293.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2002-351888/38.
DR   N-PSDB; ABK69573.
XX
PT   New mite allergenic protein isolated from Dermatophagoides, designated
PT   Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS   Claim 12; Page 120-122; 161pp; English.
XX
CC   The invention relates to an isolated mite allergenic protein of
CC   Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC   acid. The Der HMW-map protein is useful for eliciting an immune response
CC   against Der HMW-map protein. The protein or a reagent comprising a non-
CC   proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC   cat) susceptible to or having an allergic response to a mite. A
CC   therapeutic composition is useful for desensitising a host animal to an
CC   allergic response to a mite. The DNA and protein can be used in the
CC   detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC   of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC   disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC   binding of proteins to IgE, to prevent immunocomplex formation, thus
CC   reducing hypersensitivity responses to mite allergens, and as vaccines
CC   against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC   represent Der HMW-map polypeptides of the invention
XX
SQ   Sequence 555 AA;

  Query Match             100.0%;  Score 555;  DB 5;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120

Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240

Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
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Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555


RESULT 4
AAY52525
ID   AAY52525 standard; protein; 536 AA.
XX
AC   AAY52525;
XX
DT   22-FEB-2000  (first entry)
XX
DE   House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
XX
KW   Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW   house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
KW   hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW   canine; veterinary; antibody; vaccine; immunisation.
XX
OS   Dermatophagoides farinae.
XX
PN   WO9954349-A2.
XX
PD   28-OCT-1999.
XX
PF   16-APR-1999;   99WO-US008524.
XX
PR   17-APR-1998;   98US-00062013.
PR   13-MAY-1998;   98US-0085295P.
PR   02-SEP-1998;   98US-0098909P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2000-052700/04.
DR   N-PSDB; AAZ38579, AAZ38580.
XX
PT   Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT   used to modify an animals' hypersensitivy to mite allergens.
XX
PS   Claim 3; Page 125-127; 154pp; English.
XX
CC   This sequence represents Dermatophagoides farinae mite allergen protein
CC   (map) PDerf98-536, the mature form of PDerf98-555 (AAY52523). PDerf98-536
CC   has a molecular weight of 98 kD, comprising 536 amino acids, and is a
CC   component of the Dermatophagoides farinae high molecular weight mite
CC   allergen protein (HWM-map) composition. The HMW-map composition was
CC   isolated from a D. farinae homogenate by gel filtration, with each
CC   fraction being analysed for the presence of proteins that bound to IgE
CC   present in mite-allergic dog antisera. Mite allergenic proteins and
CC   peptides, and nucleic acids encoding them, may be used in therapeutic
CC   compositions to modify an animal's hypersensitivity reaction to mite
CC   allergens. Animals that may be treated include mammals and birds,
CC   especially felines, canines, equines, humans, other pets, and work or
CC   domestic animals. The proteins or fragments may also be used to diagnose
CC   allergies via a skin test. The proteins and peptides can also be used to
CC   raise antibodies, which have a variety of potential uses. For example,
CC   they can be used as vaccines to passively immunise animals against dust
CC   mite hypersensitivity, as positive controls in test kits and as tools to
CC   recover desired dust mite allergens from a mixture of proteins
XX
SQ   Sequence 536 AA;

  Query Match             96.6%;  Score 536;  DB 3;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79
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Db          1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 60

Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139

Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199

Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259

Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319

Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379

Db        301 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 439

Db        361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 420

Qy        440 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 499

Db        421 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 480

Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555

Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536
```

RESULT 5
AAU96329
ID AAU96329 standard; protein; 536 AA.
XX
AC AAU96329;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #16.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69575.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 125-127; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 536 AA;

Query Match 96.6%; Score 536; DB 5; Length 536;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79

Db          1 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 60

Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139

Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199

Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259

Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319

Db        241 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 300

Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379

Db        301 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 360

Qy        380 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 439

Db        361 NDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTPTPTTTPTTPTTTPTTPSPT 420

Qy        440 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 499

Db        421 TPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTSTPSPTTTEHTSETPKYTTY 480

Qy        500 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 555

Db        481 VDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCPPGTIWCQEKLTCIGE 536
```

RESULT 6
AAY52535
ID AAY52535 standard; protein; 490 AA.
XX
AC AAY52535;
XX
DT 06-AUG-2003 (revised)
DT 22-FEB-2000 (first entry)
XX
DE D. pteronyssius 98 kD mite allergen protein (map) PDerp98-490.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IgE; immunoglobulin E; allergen; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
KW canine; veterinary; antibody; vaccine; immunisation.

XX
OS Dermatophagoides pteronyssinus.
XX
FH Key Location/Qualifiers
FT Modified-site 115. .117
FT /note= "Asn is N-glycosylated"
FT Modified-site 240. .242
FT /note= "Asn is N-glycosylated"
XX
PN WO9954349-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-US008524.
XX
PR 17-APR-1998; 98US-00062013.
PR 13-MAY-1998; 98US-0085295P.
PR 02-SEP-1998; 98US-0098909P.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2000-052700/04.
DR N-PSDB; AAZ38589, AAZ38590.
XX
PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animals' hypersensitivy to mite allergens.
XX
PS Claim 3; Page 147-149; 154pp; English.
XX
CC This sequence represents Dermatophagoides pteronyssius mite allergen
CC protein (map) PDerp98-490, the mature form of pDerp98-509. PDerp98-490
CC has a molecular weight of 98 kD, comprising 490 amino acids, and has a
CC high degree of homology with the D. farinae mature 98 kD allergen, mapB
CC (AAY52525). Nucleic acid molecules encoding PDerp98-490 were isolated
CC from a D. pteronyssius cDNA library by hybridisation with a probe
CC encoding the D. farinae high molecular weight map (HMW-map) composition.
CC Mite allergenic proteins and peptides, and nucleic acids encoding them,
CC may be used in therapeutic compositions to modify an animal's
CC hypersensitivity reaction to mite allergens. Animals that may be treated
CC include mammals and birds, especially felines, canines, equines, humans,
CC other pets, and work or domestic animals. The proteins or fragments may
CC also be used to diagnose allergies via a skin test. The proteins and
CC peptides can also be used to raise antibodies, which have a variety of
CC potential uses. For example, they can be used as vaccines to passively
CC immunise animals against dust mite hypersensitivity, as positive controls
CC in test kits and as tools to recover desired dust mite allergens from a
CC mixture of proteins. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 490 AA;

Query Match 11.5%; Score 64; DB 3; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 292 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 351

Qy 371 SGVM 374
||||
Db 352 SGVM 355

RESULT 7
AAU96339
ID AAU96339 standard; protein; 490 AA.
XX
AC AAU96339;
XX
DT 15-JUL-2002 (first entry)
XX
DE Der HMW-map polypeptide #26.
XX
KW Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW mite allergenic protein; immunoglobulin E; hypersensitivity;
KW immunocomplex formation.
XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69585.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 144-146; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 490 AA;

Query Match 11.5%; Score 64; DB 5; Length 490;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 292 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 351

Qy 371 SGVM 374
||||
Db 352 SGVM 355

RESULT 8
AAY52533
ID AAY52533 standard; protein; 509 AA.
XX
AC AAY52533;
XX
DT 06-AUG-2003 (revised)
DT 22-FEB-2000 (first entry)
XX
DE D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509.
XX
KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
KW house dust mite; IgE; immunoglobulin E; allergen; mapB;
KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

```
KW   canine; veterinary; antibody; vaccine; immunisation.
XX
OS   Dermatophagoides pteronyssinus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /note= "Signal peptide"
FT   Protein         20. .509
FT                   /note= "Mature PDerp98-509"
XX
PN   WO9954349-A2.
XX
PD   28-OCT-1999.
XX
PF   16-APR-1999;   99WO-US008524.
XX
PR   17-APR-1998;   98US-00062013.
PR   13-MAY-1998;   98US-0085295P.
PR   02-SEP-1998;   98US-0098909P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2000-052700/04.
DR   N-PSDB; AAZ38585, AAZ38586, AAZ38587, AAZ38588.
XX
PT   Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT   used to modify an animals' hypersensitivy to mite allergens.
XX
PS   Claim 3; Page 134-136; 154pp; English.
XX
CC   This sequence represents Dermatophagoides pteronyssius mite allergen
CC   protein (map) PDerp98-509. PDerp98-509 has a molecular weight of 98 kD,
CC   comprising 509 amino acids, and has a high degree of homology with the D.
CC   farinae 98 kD allergen, mapB (AAY52523). Nucleic acid molecules encoding
CC   PDerp98-509 were isolated from a D. pteronyssius cDNA library by
CC   hybridisation with a probe encoding the D. farinae high molecular weight
CC   map (HMW-map) composition. Mite allergenic proteins and peptides, and
CC   nucleic acids encoding them, may be used in therapeutic compositions to
CC   modify an animal's hypersensitivity reaction to mite allergens. Animals
CC   that may be treated include mammals and birds, especially felines,
CC   canines, equines, humans, other pets, and work or domestic animals. The
CC   proteins or fragments may also be used to diagnose allergies via a skin
CC   test. The proteins and peptides can also be used to raise antibodies,
CC   which have a variety of potential uses. For example, they can be used as
CC   vaccines to passively immunise animals against dust mite
CC   hypersensitivity, as positive controls in test kits and as tools to
CC   recover desired dust mite allergens from a mixture of proteins. (Updated
CC   on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 509 AA;

  Query Match             11.5%;  Score 64;  DB 3;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-56;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370

Qy        371 SGVM 374
              ||||
Db        371 SGVM 374


RESULT 9
AAU96337
ID   AAU96337 standard; protein; 509 AA.
XX
AC   AAU96337;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Der HMW-map polypeptide #24.
XX
KW   Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW   mite allergenic protein; immunoglobulin E; hypersensitivity;
KW   immunocomplex formation.
XX
OS   Dermatophagoides farinae.
XX
PN   WO200222807-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028730.
XX
PR   14-SEP-2000; 2000US-00662293.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Mccall CA,  Hunter SW,  Weber ER;
XX
DR   WPI; 2002-351888/38.
DR   N-PSDB; ABK69581.
XX
PT   New mite allergenic protein isolated from Dermatophagoides, designated
PT   Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS   Claim 12; Page 134-136; 161pp; English.
XX
CC   The invention relates to an isolated mite allergenic protein of
CC   Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC   acid. The Der HMW-map protein is useful for eliciting an immune response
CC   against Der HMW-map protein. The protein or a reagent comprising a non-
CC   proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC   cat) susceptible to or having an allergic response to a mite. A
CC   therapeutic composition is useful for desensitising a host animal to an
CC   allergic response to a mite. The DNA and protein can be used in the
CC   detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC   of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC   disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC   binding of proteins to IgE, to prevent immunocomplex formation, thus
CC   reducing hypersensitivity responses to mite allergens, and as vaccines
CC   against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC   represent Der HMW-map polypeptides of the invention
XX
SQ   Sequence 509 AA;

  Query Match             11.5%;  Score 64;  DB 5;  Length 509;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-56;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370

Qy        371 SGVM 374
              ||||
Db        371 SGVM 374


RESULT 10
AAU96338
ID   AAU96338 standard; protein; 509 AA.
XX
AC   AAU96338;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Der HMW-map polypeptide #25.
XX
KW   Der HMW-map; American house dust mite; antiallergic; mite; IgE;
KW   mite allergenic protein; immunoglobulin E; hypersensitivity;
KW   immunocomplex formation.
```

XX
OS Dermatophagoides farinae.
XX
PN WO200222807-A2.
XX
PD 21-MAR-2002.
XX
PF 14-SEP-2001; 2001WO-US028730.
XX
PR 14-SEP-2000; 2000US-00662293.
XX
PA (HESK-) HESKA CORP.
XX
PI Mccall CA, Hunter SW, Weber ER;
XX
DR WPI; 2002-351888/38.
DR N-PSDB; ABK69583.
XX
PT New mite allergenic protein isolated from Dermatophagoides, designated
PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX
PS Claim 12; Page 139-141; 161pp; English.
XX
CC The invention relates to an isolated mite allergenic protein of
CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC acid. The Der HMW-map protein is useful for eliciting an immune response
CC against Der HMW-map protein. The protein or a reagent comprising a non-
CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC cat) susceptible to or having an allergic response to a mite. A
CC therapeutic composition is useful for desensitising a host animal to an
CC allergic response to a mite. The DNA and protein can be used in the
CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC binding of proteins to IgE, to prevent immunocomplex formation, thus
CC reducing hypersensitivity responses to mite allergens, and as vaccines
CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
CC represent Der HMW-map polypeptides of the invention
XX
SQ Sequence 509 AA;

Query Match 11.5%; Score 64; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.5e-56;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370

Qy        371 SGVM 374
              ||||
Db        371 SGVM 374
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Search completed: March 31, 2006, 15:26:54
Job time : 190 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:27:15 ; Search time 43 Seconds
(without alignments)
1241.868 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 35

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: March 31, 2006, 15:31:45
Job time : 43 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:23:54 ; Search time 237 Seconds
(without alignments)
1652.187 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 3

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	555	100.0	555	2	Q9U6R7_DERFA	Q9u6r7 dermatophag
2	64	11.5	532	2	Q4JK69_DERPT	Q4jk69 dermatophag
3	64	11.5	558	2	Q4JK70_DERPT	Q4jk70 dermatophag

ALIGNMENTS

RESULT 1
Q9U6R7_DERFA
ID Q9U6R7_DERFA PRELIMINARY; PRT; 555 AA.
AC Q9U6R7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 98kDa HDM allergen.
OS Dermatophagoides farinae (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6954;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21189488; PubMed=11292526; DOI=10.1016/S0165-2427(00)00258-0;
RA McCall C., Hunter S., Stedman K., Weber E., Hillier A., Bozic C.,
RA Rivoire B., Olivry T.;
RT "Characterization and cloning of a major high molecular weight house
RT dust mite allergen (Der f 15) for dogs.";
RL Vet. Immunol. Immunopathol. 78:231-247(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Weber E.R., Hunter S., Stedman K., McCall C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF178772; AAD52672.1; -; mRNA.
DR HSSP; Q13231; 1LG2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase_II.
DR InterPro; IPR002557; Chitin_bind_PerA.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 555 AA; 63238 MW; 0E4564A1A459B30B CRC64;

Query Match 100.0%; Score 555; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
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Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
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Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
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Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
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RESULT 2
Q4JK69_DERPT
ID Q4JK69_DERPT PRELIMINARY; PRT; 532 AA.
AC Q4JK69;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Group 15 allergen protein short isoform.
OS   Dermatophagoides pteronyssinus (House-dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC   Pyroglyphidae; Dermatophagoides.
OX   NCBI_TaxID=6956;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT   "Der p 15 0102-An isoform of the gene for Der p15 encoding a chitinase
RT   allergen from Dermatophagoides pteronyssinus.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; DQ078741; AAY84565.1; -; mRNA.
SQ   SEQUENCE   532 AA;  60953 MW;  A92BFB6C3C6498ED CRC64;

  Query Match             11.5%;  Score 64;  DB 2;  Length 532;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-57;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        371 SGVM 374
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Db        371 SGVM 374


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ID   Q4JK70_DERPT PRELIMINARY;      PRT;   558 AA.
AC   Q4JK70;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Group 15 allergen protein.
OS   Dermatophagoides pteronyssinus (House-dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC   Pyroglyphidae; Dermatophagoides.
OX   NCBI_TaxID=6956;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   O'Neil S.E., Heinrich T.K., Thomas W.R.;
RT   "Der p 15-A chitinase allergen from Dermatophagoides pteronyssinus.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; DQ078740; AAY84564.1; -; mRNA.
SQ   SEQUENCE   558 AA;  63497 MW;  3CBFD8C829D4CEB8 CRC64;

  Query Match             11.5%;  Score 64;  DB 2;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-57;
  Matches   64;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370

Qy        371 SGVM 374
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Db        371 SGVM 374


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Job time : 237 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:31:15 ; Search time 47 Seconds
(without alignments)
976.277 Million cell updates/sec

Title: US-09-662-293-15
Perfect score: 555
Sequence: 1 MKTIYAILSIMACIGLMNAS.....IMPCPPGTIWCQEKLTCIGE 555

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word Size: 35

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	555	100.0	555	2	US-09-292-225-15	Sequence 15, Appl
2	555	100.0	555	2	US-09-292-225-18	Sequence 18, Appl
3	536	96.6	536	2	US-09-292-225-21	Sequence 21, Appl
4	64	11.5	490	2	US-09-292-225-41	Sequence 41, Appl
5	64	11.5	509	2	US-09-292-225-35	Sequence 35, Appl
6	64	11.5	509	2	US-09-292-225-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-292-225-15
; Sequence 15, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-15

Query Match 100.0%; Score 555; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKTIYAILSIMACIGLMNASIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK 60

Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
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Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
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Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360

Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
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Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
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Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
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Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
              |||||||||||||||
Db        541 PGTIWCQEKLTCIGE 555
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RESULT 2
US-09-292-225-18
; Sequence 18, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02

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;  EARLIER APPLICATION NUMBER: 60/085,295
;  EARLIER FILING DATE: 1998-05-13
;  EARLIER APPLICATION NUMBER: 60/098,565
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: 09/062,013
;  EARLIER FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-09-292-225-18

  Query Match             100.0%;  Score 555;  DB 2;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  555;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CTHLMYGFAKIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWY 120
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Qy        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180
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Db        121 EGSEKYSDMAANPTYRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV 180

Qy        181 RELKDAFEPHGYLLTAAVSPGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNA 240
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Qy        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300
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Db        241 PLYKRPDETDELHTYFNVNYTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPA 300

Qy        301 KGMSPPGFISGEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC 360
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Qy        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420
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Db        361 KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP 420

Qy        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480
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Db        421 TPTTTPTTPTTTPTTPSPTTPTTTPSPTTPTTTPSPTTPTTTPSPTTPTPTTPTPAPTTS 480

Qy        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540
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Db        481 TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP 540

Qy        541 PGTIWCQEKLTCIGE 555
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Db        541 PGTIWCQEKLTCIGE 555


RESULT 3
US-09-292-225-21
; Sequence 21, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT: Hunter, Shirley Wu
;  APPLICANT: Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/09/292,225
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: 60/098,909
;  EARLIER FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/085,295
;  EARLIER FILING DATE: 1998-05-13
;  EARLIER APPLICATION NUMBER: 60/098,565
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: 09/062,013
;  EARLIER FILING DATE: 1998-04-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 536
;   TYPE: PRT
;   ORGANISM: Dermatophagoides farinae
US-09-292-225-21

  Query Match             96.6%;  Score 536;  DB 2;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 SIKRDHNDYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFKCTHLMYGFAKIDEYKYTIQ 79
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Qy         80 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 139
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Db         61 VFDPYQDDNHNSWEKRGYERFNNLRLKNPELTTMISLGGWYEGSEKYSDMAANPTYRQQF 120

Qy        140 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 199
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Db        121 IQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALVRELKDAFEPHGYLLTAAVS 180

Qy        200 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 259
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Db        181 PGKDKIDRAYDIKELNKLFDWMNVMTYDYHGGWENFYGHNAPLYKRPDETDELHTYFNVN 240

Qy        260 YTMHYYLNNGATRDKLVMGVPFYGRAWSIEDRSKLKLGDPAKGMSPPGFISGEEGVLSYI 319
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Qy        320 ELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGVSGVMVWSLE 379
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RESULT 4
US-09-292-225-41
; Sequence 41, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
;  APPLICANT: McCall, Catherine A.
;  APPLICANT: Hunter, Shirley Wu
;  APPLICANT: Weber, Eric R.
;  TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: AL-2-C3
;  CURRENT APPLICATION NUMBER: US/09/292,225
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: 60/098,909
;  EARLIER FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/085,295
;  EARLIER FILING DATE: 1998-05-13
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; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-41

Query Match 11.5%; Score 64; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
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Db 292 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 351

Qy 371 SGVM 374
||||
Db 352 SGVM 355

RESULT 5
US-09-292-225-35
; Sequence 35, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-35

Query Match 11.5%; Score 64; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370

Qy 371 SGVM 374
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Db 371 SGVM 374

RESULT 6
US-09-292-225-38
; Sequence 38, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-38

Query Match 11.5%; Score 64; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370
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Db 311 GEEGVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISCKLAFLKELGV 370

Qy 371 SGVM 374
||||
Db 371 SGVM 374

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 31, 2006, 15:43:20 ; Search time 24 Seconds
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Title: US-09-662-293-15
Perfect score: 555
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

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Job time : 24 secs